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OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:57:44 ; Search time 9057 Seconds

(without alignments)
11251.993 Million cell updates/sec

Title: US-08-917-710-1

Perfect score: 2155
Sequence: 1 CGGTCGCCGCCGCTCTAGAA.....CTAAAAAAAAAAAAAAAAAAAA 2155

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2043.2	94.8	2063	9	AF538734 Homo sapi
2	1869.2	86.7	1976	9	AF538732 Homo sapi
3	1848.2	85.8	1857	9	AF167343 Homo sapi
4	1538.8	71.4	1561	9	BC053621 Homo sapi
5	1242.8	57.7	4724	9	AB006537 Homo sapi
6	1242.8	57.7	4726	6	CO715161 Homo sapi
7	1096.6	50.9	4575	9	AF538730 Homo sapi
8	1068.8	49.6	4637	9	AF538733 Homo sapi
9	1056.8	49.0	1740	6	AR166115 Sequence
10	1047.8	48.6	1713	6	AX616663 Sequence
11	1047.8	48.6	2064	6	AX704564 Sequence
12	1047.8	48.6	2064	6	BD31181 Antagonis
13	1043.8	48.4	2733	6	BD31181 Antagonis
14	1043.8	48.4	2733	6	BD31181 Antagonis
15	1043.8	48.4	2733	6	BD31181 Antagonis
16	1020.8	47.3	1822	9	AX503601 Sequence
17	1020.8	47.3	1822	9	AX503601 Sequence
18	1019.2	47.3	1822	9	AX503601 Sequence
19	935	43.4	3080	9	AF167340 Homo sapi

20	930.2	43.2	184203	9	AC008249 Homo sapi
21	922.6	42.8	4488	9	AF538731 Homo sapi
22	891.8	41.4	1916	10	BC021159 Mus muscu
23	794.2	36.9	3355	6	AR166116 Sequence
24	794.2	36.9	3355	6	AX683050 Sequence
25	794.2	36.9	3355	6	AX85999 M. musculus
26	790.2	36.7	2058	10	MM1LRACP
27	783	36.3	1862	10	AX704566 Sequence
28	595.8	27.6	601	11	U48592 Rattus norv
29	447	20.7	1408	5	BV184131 Sperm14321
30	447	20.7	1456	5	CR353678 Gallus ga
31	442.8	20.5	642	10	AB079119 Rattus no
32	367.4	17.0	443	6	AB079119 Rattus no
33	281.2	13.5	880	6	AX109972 Sequence
34	285.4	13.2	287	6	FI67333804
35	285.4	13.2	287	6	FI67333804
36	249.4	11.6	16161	2	CO078673 Sequence
37	246.6	11.4	272085	2	CO078673 Sequence
38	232.8	10.8	729	11	AC119283 Sequence
39	223.6	10.4	271	6	AC098400 Rattus no
40	218.4	10.1	478	6	BV019633 S212P6158
41	218.4	10.1	478	6	AX10606 Sequence
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43	199	9.2	548	9	CO065416 Sequence
44	168	7.8	311	9	AF016261 Homo sapi
45	167.4	7.8	169	6	AF167337 Homo sapi

ALIGNMENTS

RESULT 1	AF538734	2063 bp	mRNA	linear	PRI 28-JUL-2003
LOCUS	AF538734				
DEFINITION	Homo sapiens clone L2 soluble interleukin-1 receptor accessory				
ACCESSION	AF538734				
VERSION	AF538734.1	GI:33286880			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Jensen, L.E. and Whitehead, A.S.				
TITLE	Expression of alternatively spliced interleukin-1 receptor				
JOURNAL	Cell. Signal. 15 (8), 793-802 (2003)				
MEDLINE	12781872				
PUBMED	22664804				
REFERENCE	2 (bases 1 to 2063)				
AUTHORS	Jensen, L.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-AUG-2002) Department of Pharmacology, University of				
FEATURES					
source	1..2063				
5'UTR	118..119				
misc_feature	205..206				
misc_feature	207..1277				
CDS	1..1277				
note="alternative splice site for exon 1 and exon 2"					
note="alternative splice site for exon 2 and exon 3"					
note="sili-IRAP; alternatively spliced"					
/codon_start=1					
/product="soluble interleukin-1 receptor accessory					

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Qy 2016 AAAAAGAAATCATTTAATTTATGATTTTAAATGATATACACATGATTTCTATGTGATA 2075

Db 1920 AAAAAGAAATCATTTAATTTATGATTTTAAATGATATACACATGATTTCTATGTGATA 1979

Qy 2076 GTACATATATTTATTTACATTAATGAAATTAATAAGCCTTCTGTGAGAAAGTGCTGCTC 2135

Db 1980 GTACATATATTTATTTCTACATTAATGAAATTAATAAGCCTTCTGTGAGAAAGTGCTGCTC 2039

Qy 2136 CTAATAAAAAAAAAAAAAA 2155

Db 2040 CTAATAAAAAAAAAAAAAA 2059

RESULT 2

AF538732 1976 bp mRNA linear PRI 28-JUL-2003

LOCUS

DEFINITION Homo sapiens clone L1 soluble interleukin-1 receptor accessory

ACCESSION AF538732

VERSION AF538732.1 GI:33286876

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1976)

AUTHORS Jensen, L.E. and Whitehead, A.S.

TITLE Expression of alternatively spliced interleukin-1 receptor accessory protein mRNAs is differentially regulated during inflammation and apoptosis

JOURNAL Cell. Signal. 15 (8), 793-802 (2003)

MEDLINE 12781872

PUBMED 22664804

2 (bases 1 to 1976)

Jensen, L.E.

Direct Submission

Submitted (19-AUG-2002) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104-6084, USA

FEATURES

source

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/mol_type="mRNA"

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118..119

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CDS

120..1190

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misc_feature

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/note="alternative splice site for exon 9 and exon 10"

3'UTR

1191..1954

polyA_signal

1910..1915

ORIGIN

Query Match 86.7%; Score 1869.2; DB 9; Length 1976;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 1969; Conservative 0; Mismatches 3; Indels 88; Gaps 1;

Qy 96 TGGCGGATCCAGTCTCCGCGGGTCCGCTTTGGCCAGAGGCGGGAGAGAGAGGCGCC 155

Db 1 TGGCGGATCCAGTCTCCGCGGGTCCGCTTTGGCCAGAGGCGGGAGAGAGAGGCGCC 60

Qy 156 GCGACACTGACCCATCCCGGCTGCTTTGCTGCGCCCTCTGAGCTTCCAGAAAGGC 215

Db 61 GCGACACTGACCCATCCCGGCTGCTTTGCTGCGCCCTCTGAGCTTCCAGAAAGGC 114

Qy 216 ATGTCATGTATCATCATCTTAAGAACTAGACATAGAGGCCCTTAGAGCCTCATC 275

Db 115 ----- 114

Qy 276 TTGGCCCTCCCTTAATATCTCAAGAGTACACTTCTGAGTGTGATGAGTCTTAC 335

Db 115 -----AAAGATGACACTTCTGTGATGTATGATGATCTTAC 152

Qy 336 TTTTATGAAATCTCGAAGATGATGCTCGAAGCGCTGCGATGATGCGGACCTAGACCC 395

Db 153 TTTTATGAAATCTCGAAGATGATGCTCGAAGCGCTGCGATGATGCGGACCTAGACACC 212

Qy 396 ATGAGCAATCCAGTGTGATGATGAGCCAGCTCGATCAAGTCCCACTCTTGA 455

Db 213 ATGAGCAATCCAGTGTGATGATGAGCCAGCTCGATCAAGTCCCACTCTTGA 272

Qy 456 CACTTCTTGAATTTCACTACAGACAGCCATTCAGTGGCTTACTGTGATCTGTAT 515

Db 273 CACTTCTTGAATTTCACTACAGACAGCCATTCAGTGGCTTACTGTGATCTGTAT 332

Qy 516 TGGACTAGAGAGACCGGACCTTGAGAGCCATTAATTCGCGCTCCCGAAGCCG 575

Db 333 TGGACTAGAGAGACCGGACCTTGAGAGCCATTAATTCGCGCTCCCGAAGCCG 392

Qy 576 ATTAGTAGAGAGAGATGTGCTGTGCTCCGCGCCAGCTCTCTCATATGACATGCAAC 635

Db 393 ATTAGTAGAGAGAGATGTGCTGTGCTCCGCGCCAGCTCTCTCATATGACATGCAAC 452

Qy 636 TATACCTGATGTTAAGAACTATACATATGAGCAAAAGTTGATTTCCCTTGAAGTT 695

Db 453 TATACCTGATGTTAAGAACTATACATATGAGCAAAAGTTGATTTCCCTTGAAGTT 512

Qy 696 GTTCAAAAAGACGCTGTTCAATTCGCCCATGAACTCCCATGATGATTAACGTATTA 755

Db 513 GTTCAAAAAGACGCTGTTCAATTCGCCCATGAACTCCCATGATGATTAACGTATTA 572

Qy 756 GAATATGACATTCAGAGATCACTTGTCCAAATGATGATGATATTTCTCCAGTGTG 815

Db 573 GAATATGACATTCAGAGATCACTTGTCCAAATGATGATGATATTTCTCCAGTGTG 632

Qy 816 AAACCGATATCACTTGTATATGAGCTGTATATAATACAGATTTTATATATGTAAT 875

Db 633 AAACCGATATCACTTGTATATGAGCTGTATATAATACAGATTTTATATATGTAAT 692

Qy 876 CCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 935

Db 693 CCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 752

Qy 936 TGTGTTGTTATCATATCCAGAAATGAGACGTGATCTCATCTCACAGACTGACTGTA 995

Db 753 TGTGTTGTTATCATATCCAGAAATGAGACGTGATCTCATCTCACAGACTGACTGTA 812

Qy 996 AAGTGTAGTGGCTCTCCAAAAATGAGAGCCCGCTGATCCATCAGCTATGATGAT 1055

Db 813 AAGTGTAGTGGCTCTCCAAAAATGAGAGCCCGCTGATCCATCAGCTATGATGAT 812

Qy 1056 GTGATCTATGAGAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1115

Db 873 GTGATCTATGAGAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 932

Qy 1116 TTTCTGATGATTTCTGGCAATGAGTTTGTGTGAGCACTTGAAGAAAAAAGCTGATGAC 1175

Db 933 TTTCTGATGATTTCTGGCAATGAGTTTGTGTGAGCACTTGAAGAAAAAAGCTGATGAC 992

Db	241	GAGCCAAATTAACTTCGCTCCCGAGAAACCGCATTAAGTAAAGAAAGATGTGCTGG	300
Qy	603	TTCCGAGCCCACTCTCCTCAATGACACTGGCACTACTACCTGTGATAGGAACTACA	662
Db	301	TTCCGAGCCCACTCTCCTCAATGACACTGGCACTACTACCTGTGATAGGAACTACA	360
Qy	663	TATTCAGCAAAAGTTGCATTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCATTC	722
Db	361	TATTCAGCAAAAGTTGCATTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCATTC	420
Qy	723	CCCAATGTAAGTATTTCTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCATTC	782
Db	421	CCCAATGTAAGTATTTCTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCATTC	480
Qy	783	CCCAATGTAAGTATTTCTTCCCTTGAAGTTGTTCAAAAGACAGCTGTTCATTC	842
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Qy	843	TGTTTAAATACAGATTTTAAATATGTAATACCGAAGGTATCACTTGAGTTCTC	902
Db	541	TGTTTAAATACAGATTTTAAATATGTAATACCGAAGGTATCACTTGAGTTCTC	600
Qy	903	ATTGCTTAATTTCAATTAATGAAATTAACATGTGTTGTAATATCCAGAAATGA	962
Db	601	ATTGCTTAATTTCAATTAATGAAATTAACATGTGTTGTAATATCCAGAAATGA	660
Qy	963	CGTACGTTTCATCTCAGCAGAGCTCTGACTGTAAGGTATGAAGCTCTCCAAAATGCA	1022
Db	661	CGTACGTTTCATCTCAGCAGAGCTCTGACTGTAAGGTATGAAGCTCTCCAAAATGCA	720
Qy	1023	GTGCCCCCTGTGATCCATTCACCTAATGATCATGTCGTATGAGAAAGACCGAGAG	1082
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Qy	1083	GAGCTACTCATTCCTCGTACGCTATTTAGTTTCTGATGATGATTCGCAATGAGTT	1142
Db	781	GAGCTACTCATTCCTCGTACGCTATTTAGTTTCTGATGATGATTCGCAATGAGTT	840
Qy	1143	TGCTGAGCATTGATGAGAAAAAACCTGATGATCATCTATTGATGATCACTTAACAA	1202
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Qy	1203	AGTATAGTCATAGTAGAAGCAAGATGAACTAGAACTGATGATGATGATGATGATG	1262
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Qy	1323	GTTCGCAAGCAAGCAAGATGAGCAAGAAAGTATAGTGGCTGATGATGATGATGATG	1382
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Db	1201	ATGAAAGTTTCATCTATAGTAGAATCAAAATTTGTTCTGATATTTGTTAGACCGT	1260
Qy	1563	AATGCCCAATGTAGCTTAAATAATCGACGTGATGACAGTGAACAAATTTGTCTG	1622
Db	1261	AATGCCCAATGTAGCTTAAATAATCGACGTGATGACAGTGAACAAATTTGTCTG	1320
Qy	1623	TACATTTTGAATAATTAATAAAGAAATATATCAAGGTACCAAGATGAGAAAGAC	1682
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Qy	1683	TGTTAGAGCCACATATTGTTGTAATTTAATTAAGACCCCTTTAAATCATCATGGTAG	1742
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Db	1801	AATATTAAGCCTTTCTTGTGAGAGTGTGCTCTTAAATTAATTAATTAATTAATTA	1853
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BC053621			
LOCUS			
DEFINITION			
Homo sapiens interleukin 1 receptor accessory protein, transcript			
variant 2, mRNA (CDNA clone MGC:61532 IMAGE:6160894), complete cds.			
BC053621			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 1561)			
REFERENCE			
AUTHORS			
Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,			
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,			
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,			
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,			
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,			
Sapich, T.M., Soares, M.B., Bonaldo, W.F., Casavari, T.L.,			
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,			
Carninci, P., Prange, C., Raha, S.S., Loughran, N.A., Peters, G.J.,			
Abrams, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,			
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,			
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W.,			
Villalón, D.R., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,			
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,			
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,			
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,			
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,			
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Small, D.E.,			
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
Generation and initial analysis of more than 15,000 full-length			
human and mouse cDNA sequences			
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
Direct Submission			

JOURNAL

Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Scantirip, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., H. and Green, B.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>
Series: IPAK Plate: 115 Row: m Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2430220.

FEATURES

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1..1561
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CDS

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RSAGEVAKAAKVKQKNCRCGO"

ORIGIN

Query Match 71.4%; Score 1538.8; DB 9; Length 1561;
Best Local Similarity 99.5%; Pred. No. 1.1e-310;
Matches 1554; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 92 AGACTGCCGGATCCAGGTCCTCCGGGTCCTGCTTGGCCAGAGCGCGGAGAGACAGT 151
Db 1 AGACTGCCGGATCCAGGTCCTCCGGGTCCTGCTTGGCCAGAGCGCGGAGAGACAGT 60
QY 152 GCCCGGCGACCTGACCCATCCCGGCTGCTTTTCTGCGCCCTTCTACGTTCCCAAGA 211
Db 61 GCCCGGCGACCTGACCCATCCCGGCTGCTTTTCTGCGCCCTTCTACGTTCCCAAGA 120

QY 212 AGGCATGCGCATGTATGATCATCCTAAGAACTAGAAATCGAGAGCCCTTAGAGCCCTC 271
Db 121 AGGCATGCGCATGTATGATCATCCTAAGAACTAGAAATCGAGAGCCCTTAGAGCCCTC 179
QY 272 ACTCTGCCCCCTCCCTTTAATATCTCAAGAGTGAACCTTGTGTGTGTATGATGCT 331
Db 180 ACTCTGCCCCCTCCCTTTAATATCTCAAGAGTGAACCTTGTGTGTGTATGATGCT 239
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 DEFINITION complete cds.

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 VERSION AB006537.1 GI:3041772
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (sites)
 Saito, T. and Seki, N.
 Molecular cloning of human interleukin 1 receptor accessory protein
 Unpublished
 2 (bases 1 to 4724)
 Saito, T.
 Direct Submission
 Submitted (12-AUG-1997) Yoshiyuki Saito, National Institute of
 Radiological Sciences, Genome Research Group, Anagawa 4-9-1, Inage,
 Chiba 263, Japan (E-mail: t_saito@nirs.go.jp, Tel: 043-206-3155,
 Fax: 043-251-9818)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 4575)
Jensen, L.E. and Whitehead, A.S.
Expression of alternatively spliced interleukin-1 receptor accessory protein mRNAs is differentially regulated during inflammation and apoptosis
Cell. Signal. 15 (8), 793-802 (2003)
JOURNAL 22664804
MEDLINE 12781872
PubMed 12781872
2 (bases 1 to 4575)
Jensen, L.E.
Direct Submission
Submitted (19-AUG-2002) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104-6084, USA
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207. 1247
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AF538733
ACCESSION
AF538733.1
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 4637)
Jensen, L.E. and Whitehead, A.S.
Expression of alternatively spliced interleukin-1 receptor accessory protein mRNAs is differentially regulated during inflammation and apoptosis

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Job time : 9066 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:53:49 ; Search time 1036 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2017.6	93.6	2035	10	ADF90863 Human hep
3	1242.8	57.7	4724	10	AAD51467 IL-1 rece
4	1242.8	57.7	4724	12	ADP13278 Renal cel
5	1056.8	49.0	1740	5	AA15608 Human int
6	1047.8	48.6	1713	8	ABX12862 DNA encod
7	1047.8	48.5	2064	6	ABQ81182 Human IL-
8	1046.2	48.5	1077	2	AAT32027 Soluble I
9	1046.2	48.5	1077	2	ACC48599 Soluble I
10	1046.2	48.5	1713	9	AAT32026 Human int
11	1046.2	48.5	1713	9	ACC48598 Human int
12	1043	48.4	2703	10	AAD63748 Human IL-
13	1043	48.4	2709	10	AAD63750 Human IL-
14	1043	48.4	2709	10	AAD63772 Human IL-
15	1043	48.4	2709	10	AAD63749 Human IL-
16	1043	48.4	2715	10	AAD63774 Human IL-
17	1043	48.4	2715	10	AAD63773 Human IL-
18	1043	48.4	2733	3	AA09048 Fusion po
19	1043	48.4	2733	10	AAD63742 Human cyt
20	1043	48.4	2748	10	AAD63754 Human IL-
21	1043	48.4	2754	10	AAD63755 Human IL-

22	1043	48.4	2754	10	AAD63756 Human IL-
23	1043	48.4	2754	10	AAD63778 Human IL-
24	1043	48.4	2754	10	AAD63779 Human IL-
25	1043	48.4	2760	10	AAD63780 Human IL-
26	1041.4	48.3	2703	10	AAD63760 Human IL-
27	1041.4	48.3	2709	10	AAD63761 Human IL-
28	1041.4	48.3	2709	10	AAD63762 Human IL-
29	1041.4	48.3	2748	10	AAD63766 Human IL-
30	1041.4	48.3	2754	10	AAD63767 Human IL-
31	1041.4	48.3	2754	10	AAD63768 Human IL-
32	988.8	45.9	2748	10	AAD63751 Human IL-
33	988.8	45.9	2754	10	AAD63753 Human IL-
34	988.8	45.9	2754	10	AAD63752 Human IL-
35	987.8	45.8	2703	10	AAD63745 Human IL-
36	987.8	45.8	2709	10	AAD63769 Human IL-
37	987.8	45.8	2709	10	AAD63746 Human IL-
38	987.8	45.8	2709	10	AAD63747 Human IL-
39	987.8	45.8	2715	10	AAD63770 Human IL-
40	987.8	45.8	2715	10	AAD63771 Human IL-
41	987.8	45.8	2754	10	AAD63775 Human IL-
42	987.8	45.8	2760	10	AAD63776 Human IL-
43	987.8	45.8	2760	10	AAD63777 Human IL-
44	987.2	45.8	2748	10	AAD63763 Human IL-
45	987.2	45.8	2754	10	AAD63765 Human IL-

ALIGNMENTS

RESULT 1
AAV23659 standard, cDNA, 2155 BP.
AC AAV23659;
DT 17-AUG-1998 (first entry)
XX Human interleukin-1 receptor accessory molecule cDNA.
DE Human interleukin-1 receptor accessory molecule cDNA.
XX Interleukin-1 receptor accessory molecule; IL-1R ACW; human;
KM signal transduction; infection; septic shock; inflammation;
KM rheumatoid arthritis; therapy; ds.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 303..1373
FT /*tag= a
FT sig_peptide 303..353
FT /*tag= b
FT mat_peptide 354..1370
FT /*tag= c
XX WO9808969-A1.
XX 05-MAR-1998.
XX 26-AUG-1996; 96WO-US013954.
XX 26-AUG-1996; 96WO-US013954.
XX 26-AUG-1996; 96WO-US013954.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Bednarik DP, Olsen HS, Rosen CA;
XX WPI, 1998-230267/20.
XX P-PSDB; AAW53897.
XX Nucleic acid encoding interleukin-1 receptor accessory protein - used for
XX therapeutic modulation of IL-1 activity.
XX Claim 2, Fig 1, 95pp, English.
XX

Db 1801 TGACAAATACGAAAGGAATTATATACCTTTTATATATATATGAAACATTAATCTGTA 1860
 QY 1861 GTTGTAAACATTATTAATAGCAGCCATCCAAATTTGATGC-AACTAATTAAGGTAATTGA 1919
 Db 1861 GTTGT-AAACATTAATTAATAGCAGCCATCCAAATTTGATGC-AACTAATTAAGGTAATTGA 1919
 QY 1920 TGTATTTTCCAAAATGACATATATATATATATATATTAACACATGATCATATATT 1979
 Db 1920 TGTATTTTCCAAAATGACATATATATATATATATATATTAACACATGATCATATATT 1979
 QY 1980 AAGCAGGTTATATATATACAGCAGCCACAAATGCTAAATGAAAATCATTTAAATTATG 2039
 Db 1980 AAGCAGGTTATATATATACAGCAGCCACAAATGCTAAATGAAAATCATTTAAATTATG 2039
 QY 2040 ATTTTAAATGATACATGATTTCTATGATGATGATGATGATGATGATGATGATGATGAT 2099
 Db 2040 ATTTTAAATGATACATGATTTCTATGATGATGATGATGATGATGATGATGATGATGAT 2099
 QY 2100 GGAATTTATTAAGCCTTCTGTGACAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2155
 Db 2100 GG-AATTAATTAAGCCTTCTGTGACAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2154

RESULT 2
 ADF90863
 ID ADF90863 standard; DNA; 2035 BP.
 AC ADF90863;
 XX

DT 26-FEB-2004 (first entry)
 DE Human hepatic-fibrosis disease marker SEQ ID 325.
 XX
 XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 KW hepatic carcinoma; human; de.
 XX
 OS Homo sapiens.

PN JP2003259877-A.
 XX
 PD 16-SEP-2003.

PF 11-MAR-2002; 2002JP-00065013.

PR 11-MAR-2002; 2002JP-00065013.

PA (SUMU) SUMITOMO SEIYAKU KK.

DR WPI; 2003-821598/77.

PT Hepatic fibrosis disease markers comprising polynucleotides or
 XX antibodies, useful for improved diagnosis, screening and developing drugs
 XX to treat hepatitis, to control cirrhosis and carcinoma.
 XX

PS Claim 1; SEQ ID NO 325; 313bp; Japanese.

CC The present invention relates to hepatic-fibrosis disease markers
 CC (ADP9033-ADF90871) and related proteins (ADP90872-ADP90917). The
 CC sequences are useful for detecting and treating hepatic fibrosis caused
 CC by alcohol consumption, virus infection, etc., and the associated chronic
 CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
 CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
 CC precision), so more suitable treatments can be developed and given.
 CC

XX Sequence 2035 BP; 668 A; 406 C; 395 G; 566 T; 0 U; 0 Other;

Query Match 93.6%; Score 2017.6; DB 10; Length 2035;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2031; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 102 GATCCAGTCTCCGGGGTCCGCTTTGGCCAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 161

|||||

Db 1 GATCCAGTCTCCGGGGTCCGCTTTGGCCAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 162 ACTGACCCATCCCGGCTGCTTTTGTGCGGCTCTCACTTCCAAAGAAAGCATGTGC 221
 Db 61 ACTGACCCATCCCGGCTGCTTTTGTGCGGCTCTCACTTCCAAAGAAAGCATGTGC 120
 QY 222 ATGTGATCATCACTTAAGAACTAGACATCAGCAGGCGCTTAGAAGCTCACTTTGCC 281
 Db 121 ATGTGATCATCACTTAAGAACTAGACATCAGCAGGCGCTTAGAAGCTCACTTTGCC 179
 QY 282 CTCCTTTAATATCTCAAGAGATGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 341
 Db 180 CTCCTTTAATATCTCAAGAGATGACCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 239
 QY 342 GGAATCTCGAAGTGTATGCTGAGAGCGTGGATGATCTGGGAGATGACACATAGG 401
 Db 240 GGAATCTCGAAGTGTATGCTGAGAGCGTGGATGATCTGGGAGATGACACATAGG 299
 QY 402 CAAATCCAGTGTGTAAGATGAGCCAGCTCGATCAAGTGCCTCTTTGAACTATC 461
 Db 300 CAAATCCAGTGTGTAAGATGAGCCAGCTCGATCAAGTGCCTCTTTGAACTATC 359
 QY 462 TTGAAATTCATACACACACAGCCATTCAGCTTGCTTACTGTGATCTGTATGACT 521
 Db 360 TTGAAATTCATACACACACAGCCATTCAGCTTGCTTACTGTGATCTGTATGACT 419
 QY 522 AAGCAGACCGGAGCTTGAAGAGCCCAATTAATCTCCGCTCCCGGAGAACCCATTA 581
 Db 420 AAGCAGACCGGAGCTTGAAGAGCCCAATTAATCTCCGCTCCCGGAGAACCCATTA 479
 QY 582 AAGGAGAAAGATGTCTGT 641
 Db 480 AAGGAGAAAGATGT 539
 QY 642 TGCATGTTAAGAAACATATATATGAGCAAGTGTGATTCCTTGGAGTGTTC 701
 Db 540 TGCATGTTAAGAAACATATATGAGCAAGTGTGATTCCTTGGAGTGTTC 599
 QY 702 AAGACAGCTGTTCAATTCCTCCCATGAACTCCAGTGCATTAACGTATATAGATAT 761
 Db 600 AAGACAGCTGTTCAATTCCTCCCATGAACTCCAGTGCATTAACGTATATAGATAT 659
 QY 762 GGCATTCAGAGATCACTTGTCCAATGTATGATGATATTTCTTCCAGTGTCAACCG 821
 Db 660 GGCATTCAGAGATCACTTGTCCAATGTATGATGATATTTCTTCCAGTGTCAACCG 719
 QY 822 ACTATCACTGTATATGAGCTGTATTAATAATAGAAATTTAATAATATATACCGAA 881
 Db 720 ACTATCACTGTATATGAGCTGTATTAATAATAGAAATTTAATAATATATACCGAA 779
 QY 882 GGTATGAAGTGAAGTTCTCTCATTTGCTTATTTCAATATATAGAAATTTACATGTGT 941
 Db 780 GGTATGAAGTGAAGTTCTCTCATTTGCTTATTTCAATATATAGAAATTTACATGTGT 839
 QY 942 GTTACATATCCAGAAATGAGAGCTAGCTTCACTCAACAGAGCTGTGATTAAGGTA 1001
 Db 840 GTTACATATCCAGAAATGAGAGCTAGCTTCACTCAACAGAGCTGTGATTAAGGTA 899
 QY 1002 GTAGGCTCTCCAAAATGAGAGTGCCTGTGATGCATTCACCTTAATGATGATGTC 1061
 Db 900 GTAGGCTCTCCAAAATGAGAGTGCCTGTGATGCATTCACCTTAATGATGATGTC 959
 QY 1062 TATGAGAAAGAACAGAGAGAGAGCTATCCCTGTATGAGTGTATTTATTTTCTG 1121
 Db 960 TATGAGAAAGAACAGAGAGAGAGCTATCCCTGTATGAGTGTATTTATTTTCTG 1019
 QY 1122 ATGATTTCTGCAATGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1181
 Db 1020 ATGATTTCTGCAATGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1079
 QY 1182 ATGATTTCTGCAATGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1241
 Db 1080 ATGATTTCTGCAATGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1139

QY 1242 CAGATTTGAGCATGAGAAAGTTACCTCTGAGGATCTCAAGCCAGCTATGCTGTCAT 1301
 DB 1140 CAGATTTGAGCATGAGAAAGTTACCTCTGAGGATCTCAAGCCAGCTATGCTGTCAT 1139
 QY 1302 GCTAAGATGCGCAAGGCGAAGTTGCCAAGACAGCCAGGTGAACGAGAAAGGTATAGA 1361
 DB 1200 GCTAAGATGCGCAAGGCGAAGTTGCCAAGACAGCCAGGTGAACGAGAAAGGTATAGA 1259
 QY 1362 TGGCGTCACTGATGAATCTCTCAGTCCCAATTAACATTTGCTGGAATTAAGACAAAGG 1421
 DB 1260 TGGCGTCACTGATGAATCTCTCAGTCCCAATTAACATTTGCTGGAATTAAGACAAAGG 1319
 QY 1422 AGAGATTAGAGCAAGAGAGGCTCCAGACCTAGCCCTGAGGAGCTCAACCATATGATG 1481
 DB 1320 AGAGATTAGAGCAAGAGAGGCTCCAGACCTAGCCCTGAGGAGCTCAACCATATGATG 1379
 QY 1482 AATCAAACTTAAATGAGAAATATGAAAGTTTTCATCTATGTAAGTACTCAAAATATGCT 1541
 DB 1380 AATCAAACTTAAATGAGAAATATGAAAGTTTTCATCTATGTAAGTACTCAAAATATGCT 1439
 QY 1542 TTCGATATTTGTTAGTACCGTATGCGCAATGTAGCTAAATAATGACGTGAGTACAG 1601
 DB 1440 TTCGATATTTGTTAGTACCGTATGCGCAATGTAGCTAAATAATGACGTGAGTACAG 1499
 QY 1602 TGAGACACAAATTTGCTGCTGTAACATTTATGAAAAATTAAAAACAAGAAATATTCAAA 1661
 DB 1500 TGAGACACAAATTTGCTGCTGTAACATTTATGAAAAATTAAAAACAAGAAATATTCAAA 1559
 QY 1662 GGTACCAAGATGAGAAAACTGTGAGAGCCACATATGTGTGTAATTTAAGACCTT 1721
 DB 1560 GGTACCAAGATGAGAAAACTGTGAGAGCCACATATGTGTGTAATTTAAGACCTT 1619
 QY 1722 TTTAAAAATCATTCATGCTAGAGTTTAAGAGTCAAAAAAAGATTGCTCATCTGACCTA 1781
 DB 1620 TTTAAAAATCATTCATGCTAGAGTTTAAGAGTCAAAAAAAGATTGCTCATCTGACCTA 1679
 QY 1782 AGACTTTGGGAAATTTTCTGTAACAACATTAACGAAAGGAAATTAATACCTTTAATAT 1841
 DB 1680 AGACTTTGGGAAATTTTCTGTAACAACATTAACGAAAGGAAATTAATACCTTTAATAT 1739
 QY 1842 ATTAGAAGATATCTGATGTTGTTAAACATTTATTAATAGAGCATCCATTTGTATGCA 1901
 DB 1740 ATTAGAAGATATCTGATGTTGTTAAACATTTATTAATAGAGCATCCATTTGTATGCA 1799
 QY 1902 ACTAAATTAAGGATTAATGTTATTTTCCAAAAATGCAATTAATTAATTTTAAA 1961
 DB 1800 ACTAAATTAAGGATTAATGTTATTTTCCAAAAATGCAATTAATTAATTTTAAA 1859
 QY 1962 CACTATGATGCAATTTTAAGAGGTTTAAATATACAGAGCCAGCATTTGCTAAATG 2021
 DB 1860 CACTATGATGCAATTTTAAGAGGTTTAAATATACAGAGCCAGCATTTGCTAAATG 1919
 QY 2022 AAAATCATTTAAATATGATTTTAAATGATATACATGATTTCTATGTAATGTA 2081
 DB 1920 AAAATCATTTAAATATGATTTTAAATGATATACATGATTTCTATGTAATGTA 1979
 QY 2082 TTTTATCTACAAATTAATGGAATTAATAGCTTTCTGTGAGAGGCTGCTCT 2137
 DB 1980 TTTTATCTACAAATTAATGGAATTAATAGCTTTCTGTGAGAGGCTGCTCT 2035
 RESULT 3
 AAD51467
 ID AAD51467 standard; DNA; 4724 BP.
 AC AAD51467;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE IL-1 receptor accessory protein (IL-1Rac) gene.
 XX
 KW Drug screening; fungicide; gene therapy; antibacterial; infection; IL-1;

KM virucide; interleukin-1; IL-1 receptor accessory protein; IL-1Rac; gene;
 KW de.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 207..1919
 FT /*tag= a
 FT /product= "IL-1Rac protein"
 PN
 XX
 PD W02002101015-A2.
 PD 19-DEC-2002.
 PF 11-JUN-2002; 2002W0-US018346.
 PF 11-JUN-2001; 2001US-0297305P.
 PR (INTE-) INTERLEUKIN GENETICS INC.
 PA
 XX
 PI Power S, Duff GW;
 XX
 DR WPI; 2003-148793/14.
 DR P-PSDB; AAB33567.
 XX
 PT New detection reagent, useful for monitoring molecular assembly events to
 PT permit the dissection of genetic and non-genetic influences on biological
 PT activity, comprises an interactive sensor pair.
 PS
 XX
 XX Disclosure; Fig 9; 56pp; English.
 CC The invention relates to methods, compositions and apparatus for
 CC monitoring molecular assembly events. It also relates to a detection
 CC reagent comprising an interactive sensor pair. The detection reagent is
 CC useful for monitoring molecular assembly events to permit the dissection
 CC of genetic and non-genetic influences on a particular biological
 CC activity. The method is useful for linking genetic variations to
 CC molecular and physiological events, drug screening, diagnostics, therapy
 CC selection and dosing, patient monitoring or environmental safety. The
 CC interactive sensor pairs may be used to screen for and identify novel
 CC agonists and antagonists or other molecules that modulate a biological
 CC activity. The method is also useful for selecting an appropriate targeted
 CC therapeutic for a subject having an infection, including viral, bacterial
 CC or fungal infection. It is also used in gene therapy. The present
 CC sequence is interleukin-1 receptor accessory protein (IL-1Rac) gene. This
 CC sequence is used to illustrate the method of the invention
 XX
 SQ Sequence 4724 BP; 1422 A; 902 C; 902 G; 1498 T; 0 U; 0 Other;
 Query Match 57.7%; Score 1242.8; DB 10; Length 4724;
 Best Local Similarity 99.8%; Pred. No. 1.3e-279;
 Matches 1255; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 96 TGC CGG GAT CCA GGT CTC CGG GGT CCG CTT TGG CCA GAG CGC GGA AGA GCA GTC GCC 155
 DB 1 TGC CGG GAT CCA GGT CTC CGG GGT CCG CTT TGG CCA GAG CGC GGA AGA GCA GTC GCC 60
 QY 156 GGC GAC ACG ACG ACC AAT CCG GGT GCT TTT GCT GCG CCG CTT CAG CTT CCA AAG AAG GC 215
 DB 61 GGC GAC ACG ACG ACC AAT CCG GGT GCT TTT GCT GCG CCG CTT CAG CTT CCA AAG AAG GC 120
 QY 216 ATG CTA TGA TGA TCA TCA CCA CTA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 275
 DB 121 ATG CTA TGA TGA TCA TCA CCA CTA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 179
 QY 276 TTT GCG CCG CCG CCG CTT TAT TAT CAA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 335
 DB 180 TTT GCG CCG CCG CCG CTT TAT TAT CAA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 239
 QY 336 TTT TAT GGA AT CCG TGA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 395
 DB 240 TTT TAT GGA AT CCG TGA AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG AAG 299

QY 396 ATGAGCAATCCAAAGTGTGAGATGAGCAGCTCCGATCAAGTCCCACTTTGAA 455
 DB 300 ATGAGCAATCCAAAGTGTGAGATGAGCAGCTCCGATCAAGTCCCACTTTGAA 359
 QY 456 CACTTCTTGAATTAACCTACAGCAGAGCCATTCAGCTGGCTTACTCTGATCGGAT 515
 DB 360 CACTTCTTGAATTAACCTACAGCAGAGCCATTCAGCTGGCTTACTCTGATCGGAT 419
 QY 516 TGGACTAAGCAGAGCCGAGACCTTGAGAGGCCAATTAATTCGCTCCGAGAGCCGC 575
 DB 420 TGGACTAAGCAGAGCCGAGACCTTGAGAGGCCAATTAATTCGCTCCGAGAGCCGC 479
 QY 576 ATTACTAAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 635
 DB 480 ATTACTAAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
 QY 636 TATACCTGATGTAGAGAACATCATATTGACAGCAAGTGTGATTCCTTGGAGAT 695
 DB 540 TATACCTGATGTAGAGAACATCATATTGACAGCAAGTGTGATTCCTTGGAGAT 599
 QY 636 GTTCAAAAAGACGCTGTTTCAATTCCCATGAAACTCCAGTGCAATAACTGTATTA 755
 DB 600 GTTCAAAAAGACGCTGTTTCAATTCCCATGAAACTCCAGTGCAATAACTGTATTA 659
 QY 756 GAATATGCGATTCAGAGATCATCTGTGCAATATGTAGATGATATTTCTTCCAGTGC 815
 DB 660 GAATATGCGATTCAGAGATCATCTGTGCAATATGTAGATGATATTTCTTCCAGTGC 719
 QY 816 AACCGACTATCATCTGTGTATATGAGCTGTATATATATATATATATATATATATAT 875
 DB 720 AACCGACTATCATCTGTGTATATGAGCTGTATATATATATATATATATATATATAT 779
 QY 876 CCCGAAAGTATGAACTTGTGATTTCTCATTTGCTTAAATTTAAATGAAATTTACCA 935
 DB 780 CCCGAAAGTATGAACTTGTGATTTCTCATTTGCTTAAATTTAAATGAAATTTACCA 839
 QY 936 TGTGTTGTTTACATATCCAGAAATATGAGCTAGCTTCTCACCAGAGCTGTAGTGA 995
 DB 840 TGTGTTGTTTACATATCCAGAAATATGAGCTAGCTTCTCACCAGAGCTGTAGTGA 899
 QY 996 AAGGTATGAGCTTCTCCAAAATATGAGCTGCTGCTGATTCATTCACCTAATGATCAT 1055
 DB 900 AAGGTATGAGCTTCTCCAAAATATGAGCTGCTGCTGATTCATTCACCTAATGATCAT 959
 QY 1056 GTGCTCTATGAGAAAGAACCCAGAGAGAGCTACTCTCCCTGATAGGCTATTTTGT 1115
 DB 960 GTGCTCTATGAGAAAGAACCCAGAGAGAGCTACTCTCCCTGATAGGCTATTTTGT 1019
 QY 1116 TTTCTGATGATTTCTGCAATGAGTTTGTGAGCAATGATGAGAAAAAACTGATGAC 1175
 DB 1020 TTTCTGATGATTTCTGCAATGAGTTTGTGAGCAATGATGAGAAAAAACTGATGAC 1079
 QY 1176 ATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1235
 DB 1080 ATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
 QY 1236 AGAATCAGATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1295
 DB 1140 AGAATCAGATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
 QY 1296 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
 DB 1200 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257

RESULT 4
 ADP13278
 ID ADP13278 standard; DNA; 4724 BP.
 XX ADP13278;
 AC
 XX
 DT 26-AUG-2004 (first entry)
 XX

DE Renal cell carcinoma differentially expressed gene #14.
 XX de; diagnosis; non-blood disease; solid tumor; gene expression;
 XM peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
 XX head/neck cancer; differential expression.
 OS Homo sapiens.
 XX
 PN W02004048933-A2.
 XX
 PD 10-JUN-2004.
 XX
 PR 21-NOV-2003; 2003NO-US037481.
 XX
 PR 21-NOV-2002; 2002US-0427982P.
 PR 03-APR-2003; 2003US-0459782P.
 XX
 PA (AMHP) WYETH.
 PA (TWIN) TWINE N C.
 PA (BRC) BURCZYNSKI M E.
 PA (TRIP) TREPICCHIO W L.
 PA (DORN) DORNER A.
 PA (STOV) STOVER J A.
 PA (SLON) SLONI D K.
 XX
 PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
 PI Sloni DK;
 DR WPI; 2004-460799/43.
 XX
 PT Diagnosing non-blood disease such as solid tumor, involves comparing
 PT differential expression profile of specific genes in peripheral blood
 PT sample of subject with reference expression profile of specific genes.
 XX
 PS Disclosure; SEQ ID NO 14; 350bp; English.
 XX
 CC The invention relate to a method of diagnosing (M1) non-blood disease
 CC such as solid tumor by providing peripheral blood sample of human having
 CC non-blood disease, and comparing an expression profile of specific genes
 CC in the peripheral blood sample to reference expression profile of the
 CC genes, where each of the genes is differentially expressed in peripheral
 CC blood mononuclear cells (BMNCs) of patients having the disease as
 CC compared to BMNCs of normal humans. The method is useful for diagnosing
 CC non-blood disease such as solid tumor. The solid tumor is chosen from
 CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
 CC peripheral blood sample comprises enriched PMNCs. The peripheral blood
 CC sample is a whole blood sample (claimed). (M1) is useful for identifying
 CC genes that are differentially expressed in peripheral blood samples
 CC isolated at different stages of progression, development or treatment of
 CC RCC and/or other solid tumors. This sequence corresponds to a gene that
 CC is differentially expressed and detected by the method of the invention.
 CC (Note: this sequence is not given as part of the printed specification
 CC but was obtained from NIND in electronic format at
 CC ftp://wpi./pub/published_pct_sequences).
 CC
 XX
 SQ Sequence 4724 BP; 1422 A; 902 C; 902 G; 1498 T; 0 U; 0 Other;
 Query Match 57.7%; Score 1242.8; DB 12; Length 4724;
 Best Local Similarity 99.8%; Pred. No. 1.3e-27;
 Matches 1255; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Db 96 TGGCGGATCCAGGCTCCGGGCTCGCTTGTGCGCAGAGCGGGAAGAGAGAGTGGCC 155
 1 TGGCGGATCCAGGCTCCGGGCTCGCTTGTGCGCAGAGCGGGAAGAGAGAGTGGCC 60
 QY GCGGACACTGACCCCATCCCGGCTGCTTTGTGCGCCCTTCAGTTTCCCAAGAGAGCC 215
 DB 61 GCGGACACTGACCCCATCCCGGCTGCTTTGTGCGCCCTTCAGTTTCCCAAGAGAGCC 120
 QY 216 ATGTCATGATCATCATCACTAAGAACTAGAACTAGAGAGAGAGAGAGAGAGAGAGAG 275
 DB 121 ATGTCATGATCATCATCACTAAGAACTAGAACTAGAGAGAGAGAGAGAGAGAGAGAG 179

QY	354	AGTGTGCTCGAAGACGCTGCATGACTGCGGACCTAGACACCATGAGGCAAAATCCAAAGT	413
Db	61	AGTATGCTCTGAAACGCTGCATGACTGCGGACCTAGACACCATGAGGCAAAATCCAAAGT	120
QY	414	TTTGAAGATGAGCCAGCTCGCATCAAGTGCACCTCTTTGAACACTCTTTGAATTAAC	473
Db	121	TTTGAAGATGAGCCAGCTCGCATCAAGTGCACCTCTTTGAACACTCTTTGAATTAAC	180
QY	474	TACACACAGCCCATTCAGCTGAGCCCTACTCGATCTGGTATGTGACTAAGACAGCG	533
Db	181	TACACACAGCCCATTCAGCTGAGCCCTACTCGATCTGGTATGTGACTAAGACAGCG	240
QY	534	GACCTTGAGAGCCCAATTAACTTCGCGCTCCCCGAAACCGCATTAGTAAGAGAAAGAT	593
Db	241	GACCTTGAGAGCCCAATTAACTTCGCGCTCCCCGAAACCGCATTAGTAAGAGAAAGAT	300
QY	554	GTGCTGTGCTTCGCGCCCACTCTCTCCAAATGACACTGGCACTATACCTGATGTTAAG	653
Db	301	GTGCTGTGCTTCGCGCCCACTCTCTCCAAATGACACTGGCACTATACCTGATGTTAAG	360
QY	654	AACACTACATATTGAGCAGCAAGTTGCATTCCTTGGAAGTGTTCAAAAGAACAGACTGT	713
Db	351	AACACTACATATTGAGCAGCAAGTTGCATTCCTTGGAAGTGTTCAAAAGAACAGACTGT	420
QY	714	TTCAATTCCTCCCATGAAACTCCCAAGTCATAACTGTATATGAATATGGCAATTGAG	773
Db	421	TTCAATTCCTCCCATGAAACTCCCAAGTCATAACTGTATATGAATATGGCAATTGAG	480
QY	774	ATCATTTGCCAAAGTATGATGATATTTTCTCCAGTGAACCAACGACTATGACTTGG	833
Db	481	ATCATTTGCCAAAGTATGATGATATTTTCTCCAGTGAACCAACGACTATGACTTGG	540
QY	834	TATATGGCGTGTATATAATACAGATTTTAAATGTATATCCGGAAGTATGAACCTTG	893
Db	541	TATATGGCGTGTATATAATACAGATTTTAAATGTATATCCGGAAGTATGAACCTTG	600
QY	854	AGTTTCCTCATTTGCTTAATTCCAAATAATGGAATATACACTGTGTTGTATCATATCCA	953
Db	601	AGTTTCCTCATTTGCTTAATTCCAAATAATGGAATATACACTGTGTTGTATCATATCCA	660
QY	954	GAAATGAGCGTACGTTTCATCTCACAGACCTCGACTGTAAAGTATGAGTACCTTCCA	1013
Db	661	GAAATGAGCGTACGTTTCATCTCACAGACCTCGACTGTAAAGTATGAGTACCTTCCA	720
QY	1014	AAAAATGACGTGCCCCCTGTGATCCATTCACCTTAATGATCATGTGCTTATGAGAAAGA	1073
Db	721	AAAAATGACGTGCCCCCTGTGATCCATTCACCTTAATGATCATGTGCTTATGAGAAAGA	780
QY	1074	CCAGGAGAGAGCTACCTATCCCTGTCAGCGCTATTTTATGTTTCTATGATATCTGCG	1133
Db	781	CCAGGAGAGAGCTACCTATCCCTGTCAGCGCTATTTTATGTTTCTATGATATCTGCG	840
QY	1134	AATGAGCTTTGGTGGACCATGATGGAAGAAAAAACCCTGATGACATCACTATTGATGCAAC	1193
Db	841	AATGAGCTTTGGTGGACCATGATGGAAGAAAAAACCCTGATGACATCACTATTGATGCAAC	900
QY	1194	ATTAAACGAAATATAGCTATGTTGAACAGAAATGAACCTAGAACTAGAACTGATTTTGAAC	1253
Db	901	ATTAAACGAAATATAGCTATGTTGAACAGAAATGAACCTAGAACTGATTTTGAAC	960
QY	1254	ATCAAGAAAGTTAAGCTCGAGGATCTCAAGCGCACCTATGTGTGCATGCTGGAAGTGC	1313
Db	961	ATCAAGAAAGTTAAGCTCGAGGATCTCAAGCGCACCTATGTGTGCATGCTGGAAGTGC	102
QY	1314	AAAGCGAAGTTGCCAAGCAGCCCAAGGTGAAGCAGAAAG	1353
Db	1021	AAAGCGAAGTTGCCAAGCAGCCCAAGGTGAAGCAGAAAG	1060

RESULT 6

ABX12962

XX

standard; DNA; 1713 BP.

AC		ABX12962;
XX		
DT	10-MAY-2003	(first entry)
XX		
DE	DNA encoding human soluble IL-1 receptor type 1.	
XX		
KW	Interleukin 1; human; interleukin1; IL-1; IL-1-receptor; IL-1R; ds;	
KV	IL-R accessory protein; IL-RacP; protein-protein interaction; gene.	
XX		
OS	Homo sapiens.	
XX		
PN	GB2375604-A.	
PD	20-NOV-2002.	
XX		
PF	18-MAY-2001; 2001GB-00012251.	
FR		
XX		
PA	(WARN) WARNER LAMBERT CO.	
P1	Bertelli F, Brown JP, Gee NS;	
XX		
XX	WPI, 2003-150708/15.	
DR	P-PBDB; AB008133.	
PT		
XX		
PT	Determining ability of test compound to modulate formation of interleukin	
XX	soluble trimolecular complex, by bringing into contact the components of	
XX	the complex and test compound and determining amount of complex formed.	
PS	Example 2; Page 150-151; 171pp; English.	
XX		
CC	This invention relates to a novel assay for determining the ability of a	
CC	test compound to modulate the formation of a trimolecular complex (TC)	
CC	including interleukin (IL), a soluble IL-receptor (IL-R) polypeptide and	
CC	a soluble IL-R accessory protein (IL-RacP). The method comprises bringing	
CC	into contact an IL polypeptide, a soluble IL-R polypeptide, a soluble IL-	
CC	RacP polypeptide and a test compound, and determining the amount of TC	
CC	formed. The method of the invention is useful for determining the ability	
CC	of a test compound to modulate the formation of a trimolecular complex	
CC	including IL, a soluble IL-R and a soluble IL-RacP. The method is useful	
CC	for high throughput screening and enables direct measurement of protein	
CC	binding characteristics. It is also useful for identifying small molecule	
CC	inhibitors of TC and hence of IL-1 biological activity. The method may be	
CC	used in screening methods and assays for agents which modulate the	
CC	interaction between IL and IL-R, and/or the interaction between IL-RacP	
CC	and the IL-R/IL biomolecular complexes. This method identifies small	
CC	molecule inhibitors of TC and hence IL-1 biological activity, and	
CC	provides a significant advantage over prior methods since it is possible	
CC	to does orally and to reduce the cost of production of such compounds	
CC	compared to the production cost of recombinant proteins. The main	
CC	advantage of using soluble forms of the proteins in the method is the	
CC	ease with which these reagents enable the formatting and running of High	
CC	Throughput Screening (HTS) assays. The present sequence represents a DNA	
CC	sequence encoding an interleukin 1 family protein used in the method of	
XX	the invention	
XX		
SQ	Sequence 1713 BP; 504 A; 358 C; 404 G; 447 T; 0 U; 0 Other;	
Query Match	48.6%; Score 1047.8; DB 8; Length 1713;	
Best Local Similarity	99.8%; Pred. No. 3e-234;	
Matches 1049; Conservative	0; Mismatches 2; Indels 0; Gaps 0	
OY	303 ATGACACTTCTGTGGTGTTGAAGTCTCTACTTTATGGAATCCTGCAAAGTAGATGCC	362
Db	1 ATGACACTTCTGTGGTGTTGAAGTCTCTACTTTATGGAATCCTGCAAAGTAGATGCC	60
OY	363 TCAGAAGCGTTCGATGACTGGGGACTGAGACCACTAAGGCAAAATCCAAGTGTGTAAGAT	422
Db	61 TCAGAAGCGTTCGATGACTGGGGACTGAGACCACTAAGGCAAAATCCAAGTGTGTAAGAT	120
OY	423 GAGCAGCTGCATCAAGTGGCCACTCTTTGAACAATTCTTGAATTAACATAAGCACCA	482

QY	36	TCGAAAGCGCTGCATACCTCGGGAATAGACACATGAGGCAAAATCCAAAGTGTGGAAGAT	422
Db	61	TCGAAAGCGCTGCATACCTCGGGAATAGACACATGAGGCAAAATCCAAAGTGTGGAAGAT	120
QY	423	GAGCGAGCTGCATCAAGTGCCACTCTTTGAACCTTCTGAATTCATCTACAGACA	482
Db	121	GAGCGAGCTGCATCAAGTGCCACTCTTTGAACCTTCTGAATTCATCTACAGACA	180
QY	483	GCCCATTCAGCTGCGCTTACTCTGATCTGATTTGATGATTAAGCAGGACCGGACCTTGAG	542
Db	181	GCCCATTCAGCTGCGCTTACTCTGATCTGATTTGATGATTAAGCAGGACCGGACCTTGAG	240
QY	543	GAGCCCAATTACCTCCGCTCTCCCGAAGACCGCATTAATGAAGGAAAGATGTGCTGTGG	602
Db	241	GAGCCCAATTACCTCCGCTCTCCCGAAGACCGCATTAATGAAGGAAAGATGTGCTGTGG	300
QY	603	TTCCGGCCCACTCTCCTCAATGACACTGGCAACTTACCTGCATGTTAAGAAACATCA	662
Db	301	TTCCGGCCCACTCTCCTCAATGACACTGGCAACTTACCTGCATGTTAAGAAACATCA	360
QY	663	TATTGCAAGAAAGTGCATTTCCCTTGGAGTGTCTAAAAAGACGCTTTCAATTCC	722
Db	361	TATTGCAAGAAAGTGCATTTCCCTTGGAGTGTCTAAAAAGACGCTTTCAATTCC	420
QY	723	CCCATGAACTCCCACTGCATGAATACTGATATAGAAATGAGCATTCAGAGATCACTGT	782
Db	421	CCCATGAACTCCCACTGCATGAATACTGATATAGAAATGAGCATTCAGAGATCACTGT	480
QY	783	CCAAATGATAGATATTTTCCCTTCCAGGTCAAAACCGACTATCATCTGTATATGGGC	842
Db	481	CCAAATGATAGATATTTTCCCTTCCAGGTCAAAACCGACTATCATCTGTATATGGGC	540
QY	843	TGTTATPAAAATACAGAAATTTTATATATGTAATACCCGAAGTATGAATGATTTCCCTC	902
Db	541	TGTTATPAAAATACAGAAATTTTATATATGTAATACCCGAAGTATGAATGATTTCCCTC	600
QY	903	ATTGCTTAATTTCAAAATATAGAAATTTACATATGTGTGTTACATATCCAGAAAAATGGA	962
Db	601	ATTGCTTAATTTCAAAATATAGAAATTTACATATGTGTGTTACATATCCAGAAAAATGGA	660
QY	963	CGTACGTTTCATCTCCACAGACTCTGACTGTAAAGTAGAGGCTCTCCAAAAAATGCA	1022
Db	661	CGTACGTTTCATCTCCACAGACTCTGACTGTAAAGTAGAGGCTCTCCAAAAAATGCA	720
QY	1023	GTGCCCCCTGTGATCCATTCACCTATATGATCATGTGTCTATGGAAGAAACGAGAGAG	1082
Db	721	GTGCCCCCTGTGATCCATTCACCTATATGATCATGTGTCTATGGAAGAAACGAGAGAG	780
QY	1083	GAGCTACTCAATCCCGTACGCTGATATTTTGGTTTTCGATGAGATTCGCAATGAGGTT	1142
Db	781	GAGCTACTCAATCCCGTACGCTGATATTTTGGTTTTCGATGAGATTCGCAATGAGGTT	840
QY	1143	TGCTGAGACATGATGGAATAAAACCTGATGACATCACTATGATGTACCATTAACGA	1202
Db	841	TGCTGAGACATGATGGAATAAAACCTGATGACATCACTATGATGTACCATTAACGA	900
QY	1203	AGTATATGTCATATGTAAGACACAATAATGAATCTGAACTCGATTTTGAACATCAAGAA	1262
Db	901	AGTATATGTCATATGTAAGACACAATAATGAATCTGAACTCGATTTTGAACATCAAGAA	960
QY	1263	GTTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTGTAGAACTGTGCCAAGCGAA	1322
Db	961	GTTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTGTAGAACTGTGCCAAGCGAA	1022
QY	1323	GTTGCCAAAGCAGCCAAAGGTGAAGAGAAAG	1353
Db	1021	GTTGCCAAAGCAGCCAAAGGTGAAGAGAAAG	1051

[illegible]

QY	603	TTCCGGCCCACTCTCTCTCAATGACACTGGGCACTATACCTGCAGTTTAAGGAACAATACA	662
Db	301	TTCCGGCCCACTCTCTCTCAATGACACTGGGCACTATACCTGCAGTTTAAGGAACAATACA	360
QY	663	TATTGACAGCAAGTTGCATTTCCCTGGAAATTGTTCAAATAAGACAGCTGTTTCAATTCC	722
Db	361	TATTGACAGCAAGTTGCATTTCCCTGGAAATTGTTCAAATAAGACAGCTGTTTCAATTCC	420
QY	723	CCCATGAACCTCCACAGTGCATMAACTGTATATAGAAATATGGCACTTCAGAGATCACTTGT	782
Db	421	CCCATGAACCTCCACAGTGCATMAACTGTATATAGAAATATGGCACTTCAGAGATCACTTGT	480
QY	783	CCAAATGTAGATGATTTTTCCTTCAGTGTCAAACCGACTATCACTTGGTATATGGGC	842
Db	481	CCAAATGTAGATGATTTTTCCTTCAGTGTCAAACCGACTATCACTTGGTATATGGGC	540
QY	843	TGTTATTAATAATACAGAAATTTTATATATATATATATACCCGAGGTATGAACCTTAGTTTCTC	902
Db	541	TGTTATTAATAATAAGAAATTTTATATATATATATATACCCGAGGTATGAACCTTAGTTTCTC	600
QY	903	ATTGGCTTAATTTTCAATATATGGAATATACATATGTTGTTTACATATCCAGAAATATGA	962
Db	601	ATTGGCTTAATTTTCAATATATGGAATATATACATATGTTGTTTACATATCCAGAAATATGA	660
QY	963	CGTACGTTTCATCTCACCAAGACTCTGACTGTAAAGGTATAGGCTCTCCAAAAATGCA	1022
Db	661	CGTACGTTTCATCTCACCAAGACTCTGACTGTAAAGGTATAGGCTCTCCAAAAATGCA	720
QY	1023	GTGCCCCCTGTGATCATTTCACTATGATCATGTGTCATATGAGAAAGAACCCAGAGAG	1082
Db	721	GTGCCCCCTGTGATCATTTCACTATGATCATGTGTCATATGAGAAAGAACCCAGAGAG	780
QY	1083	GAGTACTCATTCCTCGTACGGCTATTTTAGTTTCTGATGATTCCTCGAATGAGGT	1142
Db	781	GAGTACTCATTCCTCGTACGGCTATTTTAGTTTCTGATGATTCCTCGAATGAGGT	840
QY	1143	TGGTGGACCATTTGATGGAATAAAACCTGATGACATCATTTGATGTCACCATTAACGA	1202
Db	841	TGGTGGACCATTTGATGGAATAAAACCTGATGACATCATTTGATGTCACCATTAACGA	900
QY	1203	AGTATAGTCATATGATGAGAACAGAAAGATGAACCTAGAACTCAGATTTGAGCATCAAGAA	1262
Db	901	AGTATAGTCATATGATGAGAACAGAAAGATGAACCTAGAACTCAGATTTGAGCATCAAGAA	960
QY	1263	GTTTACCTCTGAGGATCTCAAGGGCAGCTATGCTGTCACTGTAGAGTGCMAAGGCCAA	1322
Db	961	GTTTACCTCTGAGGATCTCAAGGGCAGCTATGCTGTCACTGTAGAGTGCMAAGGCCAA	1020
QY	1323	GTTGCCAAAGCAGCCCAAGGTGAGGAGAAG	1353
Db	1021	GTTGCCAAAGCAGCCCAAGGTGAGGAGAAG	1051
RESULT 9			
ACCA8599			
ID	ACCA8599 standard, cDNA, 1077 BP.		
AC	ACCA8599;		
XX	11-AUG-2003 (first entry)		
DT			
XX	Soluble interleukin-1 accessory protein coding sequence.		
DE			
XX	Human; interleukin-1 accessory protein; IL-1acp; antagonist;		
XX	antiinflammatory; antirheumatic; antirheumatic; nocotropic; neuroprotective; vasotropic;		
KW	cerebroprotective; cardiac; antiinflammatory; antinflammatory; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	1..1077		
FT	/*tag= a		
FT			

Query Match	48.5%;	Score 1046.2;	DB 9;	Length 1077;
Best Local Similarity	99.7%;	Pred. No. 5.9e-234;		
Matches 1048;	Conservative	0;	Mismatches 33;	Indels 0; Gaps 0
303	ATGACACTCTGTGGGNGTGATGTGAGTGTCTACTTTATGGAATCTGCAAAATGATGCC	362		
1	ATGACACTCTGTGGGNGTGATGTGAGTGTCTACTTTATGGAATCTGCAAAATGATGCC	60		
363	TCAGAAAGCTGCGATGATGCTGGGACTAGACCAATGAGCAATCCAGTGTGTAAGT	422		
61	TCAGAAAGCTGCGATGATGCTGGGACTAGACCAATGAGCAATCCAGTGTGTAAGT	120		
423	GAGCCAGCTGCGATGCAAGGCCACTCTTTGAACAATCTTTGAATTCACATCTACAGACA	482		
121	GAGCCAGCTGCGATGCAAGGCCACTCTTTGAACAATCTTTGAATTCACATCTACAGACA	180		
483	GCCCATTCAGCTGGCTTACTCTGATCTGATTTGAACTAGACGAGCGGAGCTTTGAG	542		
181	GCCCATTCAGCTGGCTTACTCTGATCTGATTTGAACTAGACGAGCGGAGCTTTGAG	240		
543	GAGCCAAATTAATCTTCCGCTCCCCGAGAAACCGCAATTTGTAAGGAAGATGAGCTGTGG	602		
241	GAGCCAAATTAATCTTCCGCTCCCCGAGAAACCGCAATTTGTAAGGAAGATGAGCTGTGG	300		
603	TTCCGGCCCACTCTCTCATACACTGGCAATATCTGTCAGATTTAGAAACACTTACA	662		
301	TTCCGGCCCACTCTCTCATACACTGGCAATATCTGTCAGATTTAGAAACACTTACA	360		

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QY 663 TATTGACGAAAGTTGATTTCCCTTGAAGTGTGTCAAAAAGACGCTGTTCAATCC 722
DB 361 TATTGACGAAAGTTGATTTCCCTTGAAGTGTGTCAAAAAGACGCTGTTCAATCC 420
QY 723 CCCATGAACCTCCGACGATTAAGTATATAGTAATGCAATTCAGAGATACATTGT 782
DB 421 CCCATGAACCTCCGACGATTAAGTATATAGTAATGCAATTCAGAGATACATTGT 480
QY 783 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCGCATATCACTGGTATATGGGC 842
DB 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCGCATATCACTGGTATATGGGC 540
QY 843 TGTATATAATACAGAAATTTTATATATATATATATACCCGAAGTATGAATTTGCTC 902
DB 541 TGTATATAATACAGAAATTTTATATATATATATATACCCGAAGTATGAATTTGCTC 600
QY 903 ATTGCTTAATTTCAATATATGAATTAACAATGTGTTGTTACATATCCAGAAATGGA 962
DB 601 ATTGCTTAATTTCAATATATGAATTAACAATGTGTTGTTACATATCCAGAAATGGA 660
QY 963 CGTACGTTTCATCTCAGCAGAGACTCTGACTGTAAGGTATAGGCTCTCCAAAAATGCA 1022
DB 661 CGTACGTTTCATCTCAGCAGAGACTCTGACTGTAAGGTATAGGCTCTCCAAAAATGCA 720
QY 1023 GTGCCCCCTGTGATCCATTCCACTAATGATATGATGTGCTATGAGAAAGACGAGAG 1082
DB 721 GTGCCCCCTGTGATCCATTCCACTAATGATATGATGTGCTATGAGAAAGACGAGAG 780
QY 1083 GAGTACTCATTTCCCTGTACGGTCTATTTTATGTTTCTGATGATTTCTCGCAATGAGTT 1142
DB 781 GAGTACTCATTTCCCTGTACGGTCTATTTTATGTTTCTGATGATTTCTCGCAATGAGTT 840
QY 1143 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCATATTTGATGTACCATTAAGCA 1202
DB 841 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCATATTTGATGTACCATTAAGCA 900
QY 1203 AGTATAGTCATATAGTAAGACAGAAATGATGAATCTAGAACTGATTTGAGCATCAAGAA 1262
DB 901 AGTATAGTCATATAGTAAGACAGAAATGATGAATCTAGAACTGATTTGAGCATCAAGAA 960
QY 1263 GTTACCTCTGAGAGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTCCAAAGCGCA 1322
DB 961 GTTACCTCTGAGAGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTCCAAAGCGCA 1020
QY 1323 GTTGCCAAAGCAGCCAAAGGTGAAGCAAG 1353
DB 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAAG 1051

```

RESULT 10
AAT32026
ID AAT32026 standard: cDNA, 1713 BP.

AC AAT32026;
DT 14-OCT-1996 (first entry)

DE Human interleukin-1 receptor accessory protein cDNA.

KM Interleukin-1 receptor accessory protein; IL-1 antagonist; inflammation;
therapy; antiinflammatory; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT sig_peptide 1..60
FT mat_peptide /*tag= a
FT /*tag= b

XX WO9623067-A1.
XX

```

PD 01-AUG-1996.
XX
XX 17-JUN-1996; 96WO-EP000181.
XX
XX 23-JUN-1995; 95US-00376268.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Chizzonile RA, Ju GW;
XX
XX WPI; 1996-362691/36.
XX
XX P-PSDB; AAM01911.
XX
XX Isolated interleukin-1 receptor accessory protein - used to develop
XX prods. to treat or prevent inflammatory or immunological activities of
XX interleukin-1.
XX
XX Claim 2; Page 71-72; 115pp; English.
XX
XX A cDNA clone (AAT32026) codes for human interleukin-1 receptor accessory
XX protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind
XX to or otherwise activate the IL-1R, esp. the type 1 IL-1R. It was obtd.
XX from a human YT cell cDNA library using a probe derived from a human
XX partial genomic clone. The cDNA can be used for the prodn. of pure IL-1R
XX AcP by expression in a host cell. The IL-1R AcP is used to treat or
XX prevent the inflammatory or immunological activities of IL-1
XX
XX Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 U; 0 Other;
XX
Query Match 48.5%; Score 1046.2; DB 2; Length 1713;
Best Local Similarity 99.7%; Pred. No. 7.1e-234;
Matches 1048; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 303 ATGACACTTCTGTGTGTGTGATGATGATCTCTACTTTTATGGAATCCTGCAAGTATGCC 362
DB 1 ATGACACTTCTGTGTGTGTGATGATGATCTCTACTTTTATGGAATCCTGCAAGTATGCC 60
QY 363 TCAGAAAGCTGCGATGATGCGGAGCTAGACACCATGAGCAATCCAGTGTGGAAGAT 422
DB 61 TCAGAAAGCTGCGATGATGCGGAGCTAGACACCATGAGCAATCCAGTGTGGAAGAT 120
QY 423 GAGCCAGCTGCGATGATGAGTCCCACTCTTTGAACATTTCTGAATTTCAATACAGACA 482
DB 121 GAGCCAGCTGCGATGAGTCCCACTCTTTGAACATTTCTGAATTTCAATACAGACA 180
QY 483 GCCCATTCAGCTGCGCTTACTCTGATCTGATCTGATGATGAGTACGAGGACCGGACCTTGAG 542
DB 181 GCCCATTCAGCTGCGCTTACTCTGATCTGATCTGATGATGAGTACGAGGACCGGACCTTGAG 240
QY 543 GAGCCATTAATCTTCGCTCCGCTCCCGGAAACCGCATTAAGTAAGGAGAAAGTGTCTGTGG 602
DB 241 GAGCCATTAATCTTCGCTCCGCTCCCGGAAACCGCATTAAGTAAGGAGAAAGTGTCTGTGG 300
QY 603 TTCCGCGCCCACTCTCTCAATGACACTGGCACTAATACCTGCTGATTTAAGAACTATA 662
DB 301 TTCCGCGCCCACTCTCTCAATGACACTGGCACTAATACCTGCTGATTTAAGAACTATA 360
QY 663 TATTGACGAAAGTTGATTTCCCTTGAAGTGTGTCAAAAAGACGCTGTTCAATCC 722
DB 361 TATTGACGAAAGTTGATTTCCCTTGAAGTGTGTCAAAAAGACGCTGTTCAATCC 420
QY 723 CCCATGAACCTCCGACGATTAAGTATATAGTAATGCAATTCAGAGATACATTGT 782
DB 421 CCCATGAACCTCCGACGATTAAGTATATAGTAATGCAATTCAGAGATACATTGT 480
QY 783 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCGCATATCACTGGTATATGGGC 842
DB 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCGCATATCACTGGTATATGGGC 540
QY 843 TGTATATAATACAGAAATTTTATATATATATATATATACCCGAAGTATGAATTTGCTC 902
DB 541 TGTATATAATACAGAAATTTTATATATATATATATATACCCGAAGTATGAATTTGCTC 600

```

XX Disclosure; Page 33-39; 45bp; English.

CC The present sequence is the coding sequence for human interleukin-1 (IL-1)
CC 1) accessory protein (IL-1acp). The invention is based in part on the
CC discovery that soluble IL-1acp enhances the inhibitory ability of IL-1
CC receptor (IL-1R) and particularly type II IL-1R. A method is provided for
CC treating disorders associated with IL-1-mediated inflammation or IL-1
CC immunoregulatory reactions involving the administration of an IL-1
CC antagonist or inhibitor. Preferred methods use a type II IL-1R in a form
CC that binds IL-1, including IL-1 beta and IL-1 alpha, in combination with
CC IL-1acp in a form that enhances the binding of type II IL-1R to IL-1 beta
CC and IL-1 alpha. The combination results in an enhanced ability of type II
CC IL-1R to block IL-1 signal transduction, thereby interrupting the
CC proinflammatory and immunoregulatory effects of IL-1. Preferred forms of
CC IL-1acp are soluble forms such as that given in AB141899. The method can
CC be used to treat a patient afflicted with rheumatoid arthritis,
CC Alzheimer's disease, stroke, head trauma, myocardial infarction, heart
CC failure, periodontal disease, inflammatory bowel disease, asthma or
CC pancreatitis (all claimed)

XX
XX
SQ Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 U; 0 Other;

Query Match 48.5%; Score 1046.2; DB 9; Length 1713;
Best Local Similarity 99.7%; Pred. No. 71e-224;
Matches 1048; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DY 303 ATGACACTTCTGTGGTGTGTAGTAGAGTCTTACTTTTATGAAATCTGCAAAAGTAGTCC 362
1 ATGACACTTCTGTGGTGTGTAGTAGAGTCTTACTTTATGAAATCTGCAAAAGTAGTCC 60

DY 363 TCAGAAACGTGGAGATGATGGGGACTGACACCATGAGGAATTCAGTGTTAAGT 422
61 TCAGAAACGTGGAGATGAGTGGGACTGACACCATGAGGAATTCAGTGTTAAGT 120

DY 423 GAGCCAGCTCGCATCAATGCGCCACTCTTTGGAACCTTTGAAATTCACACAGACACA 482
121 GAGCCAGCTCGCATCAATGCGCCACTCTTTGGAACCTTTGAAATTCACACAGACACA 180

DY 483 GCCCATCACTGCTGCGCTTACTCTGATCTGTATGTAGCACTAAGACGCGGACCTTAG 542
181 GCCCATCACTGCTGCGCTTACTCTGATCTGTATGTAGCACTAAGACGCGGACCTTAG 240

DY 543 GAGCCATTTAATTCCGCGCTCCCGAGAACCGCACTAGTAAAGAGAAAGATGCTGTGG 602
241 GAGCCATTTAATTCCGCGCTCCCGAGAACCGCACTAGTAAAGAGAAAGATGCTGTGG 300

DY 603 TTCGGCCACTCTCTCAATGACACTGGCACTAATCTGCATGTTAAGAACTACTACA 662
301 TTCGGCCACTCTCTCAATGACACTGGCACTAATCTGCATGTTAAGAACTACTACA 360

DY 663 TATTGAGAAAGTGCATTTCCCTGGAGAGTTGTCAAAAACAGCGCTTCAATTCC 722
361 TATTGAGAAAGTGCATTTCCCTGGAGAGTTGTCAAAAACAGCGCTTCAATTCC 420

DY 723 CCCATGAACCTCCAGTGCATGAACCTGTATATGAAATATGCAATTCAGAGATCACTTGT 782
421 CCCATGAACCTCCAGTGCATGAACCTGTATATGAAATATGCAATTCAGAGATCACTTGT 480

DY 783 CCAATATGTATGATGATATTTTCTTCCAGATGCAAAACCGACTATCATCTTGATATAGGGC 842
481 CCAATATGTATGATGATATTTTCTTCCAGATGCAAAACCGACTATCATCTTGATATAGGGC 540

DY 843 TGTATATAAATAACAATTTTAAATATGTAATACCCAGAGATGAACTGAGTTCTTC 902
541 TGTATATAAATAACAATTTTAAATATGTAATACCCAGAGATGAACTGAGTTCTTC 600

DY 903 ATTGCTTAATTTCAATATGAAATTAACATGATGTTGTATCATATCCAGAAAATGGA 962
601 ATTGCTTAATTTCAATATGAAATTAACATGATGTTGTATCATATCCAGAAAATGGA 660

DY 963 CGTAGCTTCAATCCACAGAGACTGACGTGTAAGGTAGTAGGCTCTCCAAAATATGGA 1022
|||

Db	661	CGTACGTTTCACTCACACGAGACTGTACTGTAAAGGATAGGCTCTCCAAAATAATCA	720
Qy	1023	GTGCCCCCTTGATATCCATTACCTATATATCATGTGTCTATAGAAAGAACCCAGAGAG	1082
Db	721	GTGCCCCCTTGATATCCATTACCTATATATCATGTGTCTATAGAAAGAACCCAGAGAG	780
Qy	1083	GAGCTACTCATTCCTGTAGAGGTCTATTTTATGTTTCTGATGGATTTCGCGAATGAGTT	1142
Db	781	GAGCTACTCATTCCTGTAGAGGTCTATTTTATGTTTCTGATGGATTTCGCGAATGAGTT	840
Qy	1143	TGCTGACCATTTGATGGAAGAAAAACCTGATGACATCATTTGATGTCCACATTAAACGA	1202
Db	841	TGCTGACCATTTGATGGAAGAAAAACCTGATGACATCATTTGATGTCCACATTAAACGA	900
Qy	1203	AGTATTAAGTCAATAGTAAACAGAGATGAAACTGAACTCAAGATTTTGAAGATCAAGAA	1262
Db	901	AGTATTAAGTCAATAGTAAACAGAGATGAAACTGAACTCAAGATTTTGAAGATCAAGAA	960
Qy	1263	GTTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCAATGCTAAGAAAGTCCAAAGCGAA	1322
Db	961	GTTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCAATGCTAAGAAAGTCCAAAGCGAA	1020
Qy	1323	GTTTGCAAAGCAGCCAGGTGATGAGCAGAAAG	1383
Db	1021	GTTTGCAAAGCAGCCAGGTGATGAGCAGAAAG	1081

```

RESULT 12
AAB63748
ID AAB63748 standard; DNA; 2703 BP.
XX
AC AAB63748;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IL-1 Trap 823 DNA.
XX
KM Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
KM cancer; cachexia; arthritis; cytostatic; osteopathic therapy; human
XX gene; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS
FT
FT
FT
FT misc_feature
FT
FT sig_peptide
FT
FT
FT mat_peptide
FT
FT misc_feature
FT
FT misc_feature
FT
FT misc_feature
FT
FT
FT
FT
US2003143697-A1.
XX
PD 31-JUL-2003.
XX
PF 28-OCT-2002; 2002US-00262162.
XX
PR 22-SEP-1999; 99WO-US022045.
PR 22-MAR-2001; 2001US-00787835.
XX
PA (STAH/) STAH N.

```

PA	(YANC/)	YANCOPOLIOS G D.
XX		
XX	PI	Stahl N, Yancopoulos GD;
XX		
DR	WPI, 2003-851784/79.	
DR	P-PSDB, ABW02185.	
XX		
PT	New nucleic acid molecules encoding fusion polypeptides capable of	
PT	binding a cytokine to form a non-functional complex, useful for treating	
PT	cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,	
PT	or osteoporosis.	
XX		
PS	Claim 4, Fig 41, 300pp; English.	
XX		
CC	The present invention provides a novel fusion polypeptide capable of	
CC	binding a cytokine to form a nonfunctional complex. The invention is	
CC	useful for identifying agonists or antagonists of cytokine receptors and	
CC	for treating cytokine-related diseases or disorders e.g. cancer,	
CC	cachexia, arthritis and osteoporosis. The present sequence is human IL-1	
CC	trap DNA	
XX		
XX		
Sequence	2703 BP; 821 A; 627 C; 612 G; 643 T; 0 U; 0 Other;	
Query Match	48.4%; Score 1043; DB 10; Length 2703;	
Best Local Similarity	99.5%; Pred. No. 4.7e-233;	
Matches 1046;	Conservative 0; Mismatches 5; Indels 0; Gaps 0;	

Qy	303	ATGACACTTTCGATGAGTGTAGTAAAGCTCTACATTTTATGGAATTCGCAAGATGATCC	362
Db	1	ATGAGTGGTTCTGTGAGTGTGTAGTGAAGTCTACTCTTTATGGAATTCGCAAGATGATCC	60
Qy	363	TCGAAAGCGCTGGCATGAGTACTGGGGACTGACACCATTAAGGCAAAATCCAAAGTGTGAAAT	422
Db	61	TCGAAAGCGCTGGCATGAGTACTGGGGACTGACACCATTAAGGCAAAATCCAAAGTGTGAAAT	120
Qy	423	GAGCGACCTGCGCATCAAGTGGCCCACTCTTTGAAACACTCTTGAATTCMACTACAGCAC	482
Db	121	GAGCGACCTGCGCATCAAGTGGCCCACTCTTTGAAACACTCTTGAATTCMACTACAGCAC	180
Qy	483	GCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAAGCGAGACCGGACCTTGAAG	542
Db	181	GCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAAGCGAGACCGGACCTTGAAG	240
Qy	543	GAGCGATTAACTTCCCGCTCCCGGAGAACCGCACTTATGTAAGAGAAAGATGTGCTGG	602
Db	241	GAGCGATTAACTTCCCGCTCCCGGAGAACCGCACTTATGTAAGAGAAAGATGTGCTGG	300
Qy	603	TTCCGGCCCACTCTCTCTCAATGACACCTGGCACTATACCTGCAGTTTAAGAACACTACA	662
Db	301	TTCCGGCCCACTCTCTCTCAATGACACCTGGCACTATACCTGCAGTTTAAGAGCACTACA	360
Qy	663	TATGACAGCAAAAGTTGCATTTCCCTTGAAAGTTTCCAAAGAAGCAGCTGTTCAATCC	722
Db	361	TATGACAGCAAAAGTTGCATTTCCCTTGAAAGTTTCCAAAGAAGCAGCTGTTCAATCC	420
Qy	723	CCCATGAACTCCAGTGCATPAACTGTATATAGATATGCGATTTCAAGGATCACTTGT	782
Db	421	CCCATGAACTCCAGTGCATPAACTGTATATAGATATGCGATTTCAAGGATCACTTGT	480
Qy	783	CCAAATGAGATGATATTTTCCCTCCAGATGTCAAACGCACTATCACTGGTATATGGGC	842
Db	481	CCAAATGAGATGATATTTTCCCTCCAGATGTCAAACGCACTATCACTGGTATATGGGC	540
Qy	843	TGTTATATAAATACAGAAATTTTATATATGTAATACCCGAAAGTATGAATCTTGATTTCTC	902
Db	541	TGTTATATAAATACAGAAATTTTATATATGTAATACCCGAAAGTATGAATCTTGATTTCTC	600
Qy	903	ATTGCGCTTAATTTCAAAATAATGAGAAATTACACATGTGTGTTATACATATCCAGAAATATGA	962
Db	601	ATTGCGCTTAATTTCAAAATAATGAGAAATTACACATGTGTGTTATACATATCCAGAAATATGA	660
Qy	963	CGTACGTTTCACTACCGAGACTGTGACTGTAAAGTATGAGGCTTCCAAAATAATGCA	1022

Db 661 CGTAGCTTCATCTACACGAGACTGACTGTAAAGTATGAGCTCTCCAAAATGCA 720
 QY 1023 GTGCCCCCTGTATCCATTCACCTATATGATCATGTGTCTATGAGAAAACGAGAG 1082
 Db 721 GTGCCCCCTGTATCCATTCACCTATATGATCATGTGTCTATGAGAAAACGAGAG 780
 QY 1083 GAGCTACTATCCCTGTATCCCTATATTTTACTTTTGTATGATGATTTTGTATGAGTT 1142
 Db 781 GAGCTACTATCCCTGTATCCCTATATTTTACTTTTGTATGATGATTTTGTATGAGTT 840
 QY 1143 TGTGTGACCATTTGAGAAAAAACCTGTATGATCATCTATGATGATGATGATGATGAT 1202
 Db 841 TGTGTGACCATTTGAGAAAAAACCTGTATGATCATCTATGATGATGATGATGATGAT 900
 QY 1203 AGTATATGATCATATGAGAAACAGAAAGTAACTAGAACTGATTTTGTATGATGATGAT 1262
 Db 901 AGTATATGATCATATGAGAAACAGAAAGTAACTAGAACTGATTTTGTATGATGATGAT 960
 QY 1263 GTTACCTCTGAGAGATCTCAAGGCGAGCTATGCTGTATGATGATGATGATGATGAT 1322
 Db 961 GTTACCTCTGAGAGATCTCAAGGCGAGCTATGCTGTATGATGATGATGATGATGAT 1020
 QY 1323 GTTGCCAAAGCAGCCAGGCTGAGAGAAAG 1353
 Db 1021 GTTGCCAAAGCAGCCAGGCTGAGAGAAAG 1051

RESULT 14

AAD63772
 ID AAD63772 standard; DNA; 2709 BP.
 XX AAD63772;
 AC 12-FEB-2004 (first entry)
 DT 12-FEB-2004 (first entry)
 DE Human IL-1 Trap 823 mutant DNA #2.
 KW Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
 KW cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human;
 KW mutant; muteth; gene; de.
 OS Homo sapiens.
 OS Synthetic.
 PN US2003143697-A1.
 PD 31-JUL-2003.
 XX 28-OCT-2002; 2002US-00282162.
 PF 22-SEP-1999; 99MO-US022045.
 PR 22-MAR-2001; 2001US-00787835.
 XX (STAH/) STAH, N.
 PA (YANC/) YANCOPOULOS G D.
 PI Stahl N, Yancopoulos GD;
 DR WPI, 2003-851784/79.
 XX New nucleic acid molecules encoding fusion polypeptides capable of
 PT binding a cytokine to form a non-functional complex, useful for treating
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 PT or osteoporosis.
 PS Claim 38; Page; 300pp; English.
 CC The present invention provides a novel fusion polypeptide capable of
 CC binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human IL-1
 CC Trap mutant DNA. This mutant construct is obtained by insertion of bases

CC TCCGGA between the position 1077-1078 of the wild type human IL-1 trap
 CC DNA. Note: This sequence is not shown in the specification, but is
 CC derived from human wild type IL-1 Trap 823 DNA shown as SEQ ID NO: 39
 CC (Acc No: AAD63748) in figure: 41 of the specification
 XX
 SQ Sequence 2709 BP; 822 A; 629 C; 614 G; 644 T; 0 U; 0 Other;

Query Match 48.4%; Score 1043; DB 10; Length 2709;
 Best Local Similarity 99.5%; Pred. No. 4,7e-233;
 Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 303 ATGACATTTCTGCGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
 Db 1 ATGATGCTTCTGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 363 TCAAGACGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
 Db 61 TCAAGACGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 423 GAGCGACCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
 Db 121 GAGCGACCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 483 GCCCATTCAGCTGCGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 542
 Db 181 GCCCATTCAGCTGCGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 543 GAGCGAATTAATCTTCCGCTTCCCGAGAACCGGATTAAGAGAAAGTGTCTGTGG 602
 Db 241 GAGCGAATTAATCTTCCGCTTCCCGAGAACCGGATTAAGAGAAAGTGTCTGTGG 300
 QY 603 TTCCGCGCCGCTCTCTCTCAATGACCTGCACTGCACTGCACTGCACTGCACTGCACTGCA 662
 Db 301 TTCCGCGCCGCTCTCTCTCAATGACCTGCACTGCACTGCACTGCACTGCACTGCACTGCA 360
 QY 663 TATTGACGAAAGTTGATTTCCCTTGAAGTTTCAAAAAGACAGCTGTTCAATTCC 722
 Db 361 TATTGACGAAAGTTGATTTCCCTTGAAGTTTCAAAAAGACAGCTGTTCAATTCC 420
 QY 723 CCCATGAAATCTCCAGTGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 782
 Db 421 CCCATGAAATCTCCAGTGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 783 CCAATGTAGATGATGATTTTCTTCCAGGTCAAAACCGATTCATCTGATGATGATGATGAT 842
 Db 481 CCAATGTAGATGATGATTTTCTTCCAGGTCAAAACCGATTCATCTGATGATGATGATGAT 540
 QY 843 TGTATATAATACAGAAATTTAATAATGATATCCGAAAGTATGAATGATGATGATGATGAT 902
 Db 541 TGTATATAATACAGAAATTTAATAATGATATCCGAAAGTATGAATGATGATGATGATGAT 600
 QY 903 ATTGCGTTAATTTCAATAATGAAATTTACATGATGATGATGATGATGATGATGATGATGAT 962
 Db 601 ATTGCGTTAATTTCAATAATGAAATTTACATGATGATGATGATGATGATGATGATGATGAT 660
 QY 963 CGTACGTTTCAATCTCAGCAGACTGACTGTAAAGTATGATGATGATGATGATGATGATGAT 1022
 Db 661 CGTACGTTTCAATCTCAGCAGACTGACTGTAAAGTATGATGATGATGATGATGATGATGAT 720
 QY 1023 GTGCCCCCTGTATCCATTCACCTATATGATCATGTGTCTATGAGAAAACGAGAG 1082
 Db 721 GTGCCCCCTGTATCCATTCACCTATATGATCATGTGTCTATGAGAAAACGAGAG 780
 QY 1083 GAGCTACTATCCCTGTATCCCTATATTTTACTTTTGTATGATGATTTTGTATGAGTT 1142
 Db 781 GAGCTACTATCCCTGTATCCCTATATTTTACTTTTGTATGATGATTTTGTATGAGTT 840
 QY 1143 TGTGTGACCATTTGAGAAAAAACCTGTATGATCATCTATGATGATGATGATGATGATGAT 1202
 Db 841 TGTGTGACCATTTGAGAAAAAACCTGTATGATCATCTATGATGATGATGATGATGATGAT 900
 QY 1203 AGTATATGATCATATGAGAAACAGAAAGTAACTAGAACTGATTTTGTATGATGATGATGAT 1262

Db	901	AGTATAGTCATAGTAGAACAAGATGAACAGAACTCAGATTTTGACATCAAGAA	960
Qy	1263	GTTACCTTGAGGATCTCAAGCGCAGCTATGTCTGTGTCATGTAGAAAGTGC	1322
Db	961	GTTACCTTGAGGATCTCAAGCGCAGCTATGTCTGTGTCATGTAGAAAGTGC	1020
Qy	1323	GTTGCCAAGCAGCCAGGTGAAGCAGAAAG	1353
Db	1021	GTTGCCAAGCAGCCAGGTGAAGCAGAAAG	1051

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Job time : 1041 secs

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OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:58:19, Search time 185 Seconds
(without alignments)
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Title: US-08-917-710-1

Perfect score: 2155
Sequence: 1 CGGTGGCCGCTTCTAGAA.....CTAAAAAAAAAAAAAAAAAAAA 2155

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1056.8	49.0	1740	3	US-08-991-944-1
2	1043	48.4	2733	4	US-09-313-942-27
3	794.2	36.9	3355	4	US-08-991-944-3
4	133	6.2	229	4	US-09-513-999C-13178
5	102.8	4.6	2061	3	US-09-173-151A-3
6	99.4	4.5	1737	3	US-09-173-151A-1
7	97	4.3	2537	3	US-09-173-151A-34
8	66.8	3.1	2045	3	US-08-793-088A-1
9	62	2.9	1141	4	US-09-806-708B-22
10	61.4	2.8	1141	4	US-09-806-708B-22
11	57.8	2.7	680	4	US-09-489-847-73
12	57.4	2.7	2040	2	US-08-533-669A-5
13	57.4	2.7	2040	3	US-09-183-861-5
14	57.4	2.7	2040	3	US-09-022-765-5
15	57.4	2.7	2040	4	US-09-551-974A-5
16	57.4	2.7	2040	4	US-09-565-501A-5
17	57.4	2.7	2040	4	US-09-639-206A-5
18	57.4	2.7	2040	4	US-09-874-923-5
19	57.4	2.7	2040	4	US-08-798-841-5
20	57	2.6	1850	3	US-08-617-860B-32
21	57	2.6	4088	2	US-08-605-106-4
22	56.2	2.6	3089	1	US-08-472-934-5
23	56.2	2.6	3089	2	US-08-323-460A-5
24	56.2	2.6	3089	2	US-08-461-146C-5
25	56.2	2.6	3089	3	US-08-461-145C-5
26	56.2	2.6	3089	3	US-08-628-823-9
27	55.4	2.6	1774	4	US-09-489-847-17

28	55.4	2.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
29	55.2	2.6	867	4	US-09-204-865-8	Sequence 8, Appl
30	55	2.6	500	3	US-08-818-112-101	Sequence 101, App
31	55	2.6	500	3	US-08-818-111-96	Sequence 96, Appl
32	55	2.6	500	3	US-09-056-556-101	Sequence 101, App
33	55	2.6	500	4	US-09-072-596-96	Sequence 96, Appl
34	55	2.6	500	4	US-09-072-967-101	Sequence 101, App
35	55	2.6	506	3	US-09-227-357-116	Sequence 116, App
36	55	2.6	860	3	US-08-998-416-287	Sequence 287, App
37	54.4	2.5	1542	4	US-09-345-473E-13	Sequence 13, Appl
38	54.2	2.5	1378	1	US-08-075-533-20	Sequence 20, Appl
39	54.2	2.5	1378	2	US-08-948-176-20	Sequence 20, Appl
40	54.2	2.5	1378	5	PCT-US91-09160-20	Sequence 20, Appl
41	54.2	2.5	1517	4	US-09-904-615-64	Sequence 64, Appl
42	54.2	2.5	3300	4	US-09-482-273-68	Sequence 68, Appl
43	54.2	2.5	4062	4	US-09-270-767-5814	Sequence 5814, Ap
44	54.2	2.5	4062	4	US-09-270-767-21096	Sequence 21096, A
45	54	2.5	1463	4	US-09-501-115-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-08-991-944-1
; Sequence 1, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; TITLE OF INVENTION: Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991, 944
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1719
; US-08-991-944-1
;
Query Match 49.0%; Score 1056.8; DB 3; Length 1740;
Best local similarity 99.8%; Pred. No. 4.7e-283;
Matches 1059; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
TCGCAAGGATGACCTTCGTGGTGTAGTAGCTACTTTATGGAATCCCGCA 353
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[illegible]

RESULT 2
US-09-313-942-27

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? Sequence 27, Application US/09313942
? Patent No. 6472179
? GENERAL INFORMATION:
? APPLICANT: REGENERON PHARMACEUTICALS, INC.
? TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
? TITLE OF INVENTION: AND USING
? FILE REFERENCE: REG 203-A
? CURRENT APPLICATION NUMBER: US/09/313,942
? CURRENT FILING DATE: 1999-05-19
? PRIOR APPLICATION NUMBER: 09/313,942
? PRIOR FILING DATE: 1999-05-19
? PRIOR APPLICATION NUMBER: 60/101,858
? PRIOR FILING DATE: 1998-09-25
? NUMBER OF SEQ. ID NOS: 32
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 27
? LENGTH: 2733
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(2730)
? US-09-313-942-27

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	Query March	Similarity	98.4%	Score 1043;	DB 4;	Length 2733;	
	Best Local	Similarity	99.5%	Pred. No.	4-2e-279;		
	Matches 1046;	Conservative	0;	Mismatches	5;	Indels	0; Gaps 0;
QY	ATGACACTCTGTGGTGTAAGTGTCTACTTTATGGAATCCCGAAAGTGATGCC	362					
Db	1 ATGTGCTTCCTGTGTGTGTAGTAGCTCTACTCTTTATGGAATCCCGAAAGTGATGCC	60					
QY	TCACAAGCGTCGCATGACTGGGGACTGACACCATGAGGCAAAATCCTAAGTTTGAAGAT	422					
Db	61 TCGAACCGCTGCGATGACTGGGGACTGACACCATGAGGCAAAATCCTAAGTTTGAAGAT	120					
QY	GAGCAGCTGCGCATCAAAGTCCCACTTTGAAACATTCTGAAATTCATCACACACA	482					
Db	121 GAGCAGCTGCGCATCAAAGTCCCACTTTGAAACATTCTGAAATTCATCACACACA	180					
QY	GCCCCATTCAGTGGCCCTTACTGTATCGGATTTGACTAAGACGAGACCAGGACCTTGAG	542					
Db	181 GCCCATTCAGTGGCCCTTACTGTATCGGATTTGACTAAGACGAGACCAGGACCTTGAG	240					
QY	543 GAGCCCAATTAATCTTCGCTCCCGAGAACCCGATTAGTAAGAAGAAAGATGTCTGTG	602					
Db	241 GAGCCCAATTAATCTTCGCTCCCGAGAACCCGATTAGTAAGAAGAAAGATGTCTGTG	300					
QY	603 TTCGGGCCCACCTCCCTCAATGACACGTGGCACTATACCTGACATGTAAGGAACACTACA	662					
Db	301 TTCGGGCCCACCTCCCTCAATGACACGTGGCACTATACCTGACATGTAAGGAACACTACA	360					
QY	663 TATTGCAGCAAGTTGCATTTTCCCTTGGAGTTGTTCAAAAAGACAGTGTTCATTTCC	722					
Db	361 TATTGCAGCAAGTTGCATTTTCCCTTGGAGTTGTTCAAAAAGACAGTGTTCATTTCC	420					
QY	723 CCGATGGAACCTCCAGATGATAAOTGATATAGAAATGSGACTTCAGAGATCACTGT	782					
Db	421 CCGATGGAACCTCCAGATGATAAOTGATATAGAAATGSGACTTCAGAGATCACTGT	480					
QY	783 CCAATGTAGATGATATTTTCTTCCAGTGTCAAACCGACTATOCATCTGSTATATGSGC	842					
Db	481 CCAATGTAGATGATATTTTCTTCCAGTGTCAAACCGACTATOCATCTGSTATATGSGC	540					
QY	843 TGTTATTAATAATAGAAATTTTAATATATATATACCCGAAAGTATGAACTTGAAGTTCTC	902					
Db	541 TGTTATTAATAATAGAAATTTTAATATATATATATACCCGAAAGTATGAACTTGAAGTTCTC	600					
QY	903 ATTGCTTAATTTCCAAATATGAAATTACACATGTGTTTACATATCCGAAAAATGGA	962					
Db	601 ATTGCTTAATTTCCAAATATGAAATTACACATGTGTTTACATATCCGAAAAATGGA	660					
QY	963 CGTAGTTTATCTACACGAGACTCTGACTGTAAGAGTAGAGCTCCAAAAAATGCA	1022					

Db 1151 GGAAGCTGAGCAGCTGCCAAGCTGAACAGAAAG 1185

RESULT 4
US-09-513-999C-13178
Sequence 13178, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13178
LENGTH: 229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-13178

Query Match 6.2%; Score 133; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 3,8e-27;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 TCACTGGGGAGAGACTGCCGGGATCCAGGTCCTCCGGGGTCCGCTTTGGCCAGAGGCGCGGA 141
Db 1 TCACTGGGGAGAGACTGCCGGGATCCAGGTCCTCCGGGGTCCGCTTTGGCCAGAGGCGCGGA 60

QY 142 AAGAGAGAGTGGCCGGCGGACACTGACACCCATCCCGGCGCTTTGGCTGGCGCCCTCTAGC 201
Db 61 AAGAGAGAGTGGCCGGCGGACACTGACACCCATCCCGGCGCTTTGGCTGGCGCCCTCTAGC 120

QY 202 TTCCCAAGAAAG 214
Db 121 TTCCCAAGAAAG 133

RESULT 5
US-09-173-151A-3
Sequence 3, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: DMAX Research Institute
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2058
US-09-173-151A-3

Query Match 4.8%; Score 102.8; DB 3; Length 2061;
Best Local Similarity 50.9%; Pred. No. 3.5e-18;
Matches 329; Conservative 0; Mismatches 302; Indels 15; Gaps 3;

QY 313 TGTGTGTGTAGTGAAGTCTCTACTTTTATGATCACTCGAAGATGCTCGTAGAAGCT 372
Db 32 TGTGTGTGTAGTGAAGTCTCTACTTTTATGATCACTCGAAGATGCTCGTAGAAGCT 91

QY 373 GCGATGACTGGGAGCTAGACACCCATGAGGCAATCCAGTGTGTAAGTGGCCAGCTC 432
Db 92 GCGATGACTGGGAGCTAGACACCCATGAGGCAATCCAGTGTGTAAGTGGCCAGCTC 148

QY 433 GCATCAAGGCCACCTCTTGAACACTCTTGAATTCACCTACAGCAGCCCATTCAG 492
Db 149 GCATCAAGGCCACCTCTTGAACACTCTTGAATTCACCTACAGCAGCCCATTCAG 208

QY 493 CTGGCCTTACTGATCTGTATTTGGACTAAGCAGGACCGGACCTTGAGAGCCATTA 552
Db 209 CTGGCCTTACTGATCTGTATTTGGACTAAGCAGGACCGGACCTTGAGAGCCATTA 262

QY 553 ACTTCGGCCCTCCCGGAAACCGCATTAAGAGAGAAAGATGCTGTGTCGGGCCCA 612
Db 263 TCTTTT-----CAGAGGTGAGATGAGCAAGAGGAAATTCATATGTTTCACTAG 316

QY 613 CTCTCTCATGACACTGCGCACTATACCTGATGTTAAGAACATACATATTCAGCA 672
Db 317 CTGAGGCAAGACAGACTGATCTTACACTGTGTTTAAGAACATACATATTCAGCA 376

QY 673 AAGTTCATTTCCCTTGAAGTGTTCACAAAAGACAGCTTTCATTTCCCAATGAAC 732
Db 377 AAGTTCATTTCCCTTGAAGTGTTCACAAAAGACAGCTTTCATTTCCCAATGAAC 436

QY 733 TCCAGATGATAGATGATATGATATGATGATGATGATGATGATGATGATGATGATG 792
Db 437 TCCAGATGATAGATGATATGATATGATGATGATGATGATGATGATGATGATGATG 496

QY 793 ATGATATTTTCTTCAGATGCAACGACATATCACTTGATATGAGGCTGTATATAA 852

QY 906 GCGTTAATTCATATGAAATTCACATGTTGTTACATATCCAGAAA 958
 Db 595 GTTCAAGAAGATGAGAGAAATTCACATGTTGAATTAATGAGAAA 647

RESULT 7
 US-09-173-151A-34
 / Sequence 34, Application US/09173151A
 / Patent No. 6326472
 GENERAL INFORMATION:
 APPLICANT: Timans, Jacqueline C.
 APPLICANT: Debets, Johannes Eduard Maria
 APPLICANT: Antonius
 APPLICANT: Sana, Theodore R.
 APPLICANT: Bazar, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/173,151A
 FILING DATE: 14-OCT-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: CHING, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200
 INFORMATION FOR SEQ. ID NO.: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2537 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2004
 US-09-173-151A-34

Query Match

4.5%; Score 97; DB 3; Length 2537;

Best Local Similarity 49.7%; Pred. No. 1.6e-16;
 Matches 278; Conservative 0; Mismatches 275; Indels 6; Gaps 1;
 QY 396 ATGAGCAATTCAGAGTTGTTGAAGTAGAGCCAGCTCCGATTAAGTCCCACTTTGAA 455
 Db 28 ATCAAGAAATATCAAGTTTGGTGGAGAGCCCTGTCATCAATGAGCACTCTTTAT 87
 QY 456 CACTTCTGAANTCAACTACAGCAAGCCCAATTCAGCTGGCTTACTCTGATCTGAT 515
 Db 88 GGTATATACAGAACAAATTTACTCCCTGGCCCAAGTGTGATGATGATGATGATGAT 147
 QY 516 TGGACTAGACAGAGACCGGACCTTGAAGAGCCCAATTAATTCCTCGCTCCCGAGACCG 575
 Db 148 AAAAGTTCTGCTCTGAGACCTTGAAGAGCCCAATGACCT-----TTGACGGAATGAG 201
 QY 576 ATTAGTAAGAGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
 Db 202 ATGAGCAAGAGAGAGAGCTCAATTTGGTTCGCGCAACTTCTACAGAGAGTGTCTC 261
 QY 636 TATACCTGATGTTAAGAACACTACATATTCAGACAAAGTTGCAATTCCTTGAAGTT 695
 Db 262 TAGCCTGTGATACAGAACTCACTTACTGTATGAAGTATTCATCTCACTGACAGTG 321
 QY 696 GTTCAAAAAGACAGCTGTTCAATTCCTCCCAAGAACTCCAGTGCATTAATGATATA 755
 Db 322 GGTGAAAAGACAGCTGACTGCTATTAATTCAGAGTAAGTATTTGAAAAGCTGAA 381
 QY 756 GAATATGCAATTCAGAGATCACTGCTCAATTCAGAGTAAGTATTTGCTTCAAGTGC 815
 Db 382 CTAGCAAAAGCAAGAAATTTCAATGCGTGCATAGAGATTTCTACTGCAACGAGA 441
 QY 816 AAACGACTATCATCTGTTATATGAGCTGTTTAAATACAAATTTTAAATATATATA 875
 Db 442 GAACCTGAATCCTTTGTTACAGAGATGACAGACAAACATGAGGCAAGTATGTA 501
 QY 876 CCGGAGATGATGAGCTGATGTTCCATTCATTCGCTTATTCATTAATGAAATATACA 935
 Db 502 TTGAAAAGATATCTTCTTATAGAGAGTCAGAGAGATGAGATGATGAAATATATACC 561
 QY 936 TGTGTTGTTACATATCCAG 954
 Db 562 TGTGAATTAATATGAGAG 580

RESULT 8
 US-08-795-088A-1
 / Sequence 1, Application US/08795088A
 / Patent No. 6242569
 GENERAL INFORMATION:
 APPLICANT: Sui, Hong-Bing
 APPLICANT: Goeddel, David V.
 TITLE OF INVENTION: Regulators of Apoptosis
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Science & Technology Law Group
 STREET: 75 Denise Drive
 CITY: Hillsborough
 STATE: California
 COUNTRY: USA
 ZIP: 94010
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795,088A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-001

```

? TELECOMMUNICATION INFORMATION
? TELEPHONE: (650) 343-4341
?   TELEFAX: (650) 343-4342
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2045 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? IS-Org-795.-088A-1
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Query Match	3.1%;	Score 66.8;	DB 3;	Length 2045;
Best Local Similarity	68.7%;	Pred. No. 3.4e-08;		
Matches 92;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

QY	1	CGGTGGGGCCCGTTCTAGAACTAGTGATCCCCGGAGATGAGGAATTCGGCAGAA	60
Db	24	CGGGGGGGCCGCTCTTAGAACTAGTGATCCCCGGAGTGCAGGAATTCGGCAGAGC	83
QY	61	GTGCGCGGGAATATAGAGCTCACTGGGGAAGACTCGCGGATCCAGTTCGCGGGTC	120
Db	84	TTTGACGCTTCACCCAGAGTCTCACTAAAGGACTCCGAGACTAGGGTGGGACTC	143
QY	121	CGGCTTTGGCCAGAG	134
Db	144	GGCCTCACACAGTG	157

RESULT 9

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US-09-806-708B-22/c
? Sequence 22, Application US/09806708B
? Patent No. 6784342
? GENERAL INFORMATION:
? APPLICANT: The University of British Columbia
? TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
? FILE REFERENCE: 4810-58741
? CURRENT APPLICATION NUMBER: US/09/806,708B
? CURRENT FILING DATE: 2001-04-03
? PRIOR APPLICATION NUMBER: US 60/147,133
? PRIOR FILING DATE: 1999-08-04
? NUMBER OF SEQ ID NOS: 23
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 22
? LENGTH: 1141
? TYPE: DNA
? ORGANISM: Artificial sequence
? FEATURE:
? NAME/KEY: promoter
? LOCATION: (1)..(1141)
? OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

```

Query Match	2.9%;	Score 62;	DB 4;	Length 1141;
Best Local Similarity	-12.8%;	Pred. No. 5.2e-07;		
Matches 97;	Conservative 268;	Mismatches 387;	Indels 6;	Gaps 2;

QY	1366	GTCAAGTGAATCTCTCAGCTCCAAATTACATTTGTGTAAATAGGACAAAAGGAG	1425
		: : : : : : : : : : : : : : : : : : : :	
Db	1072	GTNNRWCRRYTAHTWTYRSYANNSCATXEBTWYTKMTATYTRTDYAWMCAKMRNNMWC	10131
QY	1426	ATTGAGAACAGAGAGCTCCAGCATCTGAGCGGANTCTAAACCATAGTAAATGATC	1485
		: : : : : : : : : : : : : : : : : : : :	
Db	1012	ATINYAKSCATNNNAWYATTTWAAVYAAKAKARWAGNNNRBYGAAAGNMGCAAAATMGB	953
QY	1486	AAACTTAAATGAAAATAATGAAAGTTTCATCTATGTAGATCTCAAAATATTGTTCT	1545
		: : : : : : : : : : : : : : : : : : : :	
Db	952	WMAADTAGMCCNNNNNNNTTVDVRBAMAKMKNNNNNNNAUYTACYNBPATNNKKATHHMKWTH	893
QY	1546	GATATTGTGTACCGTAATGCCCAATGTAGCTAAAAAAATCCACGCGAGTACAGTQAG	1605
		: : : : : : : : : : : : : : : : : : : :	
Db	892	GAHSKRRIHHTTRICRTKYNNNNNNAATVYWHHHAARRMNAWMTRTNNNNNNNNNNAAC	833

Oy	1606	ACACAATTGTTGCTGTACAAATATGAAAAATAAAAACAAGAAATATTCGAAGTA	1665
Dd	832	RNRTWMBAMBHSHSCNNNNNNNNNNNNNNNTMCHITTNABBCYANNNAABAARICNN	773
Oy	1666	CCAAAGATAGAAAAAATCGTAGGCCACATATTGGTGGAATTATTAGACCCTTTTA	1725
Dd	772	YMHAAYVTTTHDWCYKTMNTWTWYDDMTTBETTRMMTSTNNNNNNNNMACTNNNN	713
Oy	1726	AAATCATCTAGGTAGAGTTTAAAGTCATATAAAAAAGATGCATCATCTGACCTTAAGAC	1785
Dd	712	NNMKAYAAAHATNNWGCMWNTTDARKTNNTTWERRMNTTKTMYSTRHHHTGALTNN	653
Oy	1786	TTTCGGAATTTTCCTGAAACAATAACAGAAGGAATATATACTTTTAATATTA	1845
Dd	652	NNNNNNNNNNNNNNNSCCTCRMNTMRMTKMGDGTVTKRYKWRBTTCYVDVMADSWWW	593
Oy	1846	GAAACA-TTATCTGTACTGTGTAACCACTTTAATACAGCACCAATGATGACAACT	1904
Dd	592	YANMRCRDVITYIRANTYYCKSYAHSYWYSNNAAWTRYRSLRWSSPAKRITBRNNWWWG	533
Oy	1905	AATTAGGATTTGAATGTTTAYTTTCCAAAAATGCATPATTAATATAATATTTTAAAC	1964
Dd	532	BVRMRAGTGMWRHMNNNNNTDIRXYMMWKWARBTTTYDSMCNAKSMRRGNRRRAKKMW	473
Oy	1965	TATGTATCAATATTTAAG-----CAGGTTTATAATACAGCAGCCACATTCCTATAA	2019
Dd	472	WAANDGANDHDHYWMNGNTMMWRRAKMNWMAWCBRAJCCNNNNNRACVMEWHKMRW	413
Oy	2020	TGAAAAATCATTTAATATGATTTTAAATGATATACATGATTTCTAGTTGATAGTAC	2079
Dd	412	TMKYMWRACCNNNBKAMYRVAMMYVSBDPTNTDNMMWTSDBEWMHYTYDYWRBAMNN	353
Oy	2080	TATTTATTTCTACAAATAATGAGAAATATAAGCTTC	2117
Dd	352	NNNNNMRCBCKTISWWWNDNNHTHCYTGNNTGSAYEM	315

RESULT 10

```

US-09-806-708B-22
: Sequence 22, Application US/09806708B
: Patent No. 6784342
: GENERAL INFORMATION:
: APPLICANT: The University of British Columbia
: TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
: FILE REFERENCE: 4810-58741
: CURRENT APPLICATION NUMBER: US/09/806,708B
: CURRENT FILING DATE: 2001-04-03
: PRIOR APPLICATION NUMBER: US 60/147,133
: PRIOR FILING DATE: 1999-08-04
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: Promoter
: LOCATION: (1)..(1141)
: OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

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Query Match	2.8%	Score 61.4	DB 4	Length 1141
Best Local Similarity	11.4%	Pred. No. 7.6e-07		
Matches 114	Conservative 362	Mismatches 517	Indels 7	Gaps 2

QY 563 CCCCAGAACCCCATTTAGTAAGAGAAAGAAATGTGTGGTTCGCGCCCATCTCCCAA 622
 ::
 Db 64 MYCKYRMYNNNSRWKMKYKKKYBCKANNISBRYTHARPMWEDMTAIABMTMTNMGKGTW 123
 QY 623 TGAACGTGGCAACTTACCTGCATGTTAAGGAACACTACATATTGACGACGAAGTTGCATT 682
 ::
 Db 124 RHRYWWRMBEITVJHHYATMNNAMTTCMWDKDDKRTRWWRKNNNATGWDDTDTYHM 183

QY 693 TCCCTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATCCGCCCATGAACCTCCAGTGA 742
 Db 184 MNNNGCEIVTMMVVRKDKIDRDSBKRMMYGMBMWKNWSVDVITYYYMMVMDCKRKRYRVR 243
 QY 743 TAACTGTAATAGATATGGCATTGACAGATCATCTTGCCAAATGATGATGATATT 802
 Db 244 TGRGRMNTVMVMBTJHRRRYNNGWBTBAAVYRMTNNNNNNNAKMKCKAKYMGWVRABVN 303
 QY 863 TCCCTTCAGTGTCAAAACCGACTATCACTGGATATGAGCTGTGTATAAAATACAGAAATTT 862
 Db 304 STCTTWSKTTKVRISCTANNCRAGADANKDKHMKWSLAAGVYNNNNNNNNNTYKKARHB 363
 QY 863 TAAATGATTAATACCCGAGGATGAACTTG--AGTTTCCATGTCTTAATTTCAAAT 920
 Db 364 ARMDVMSHWKMKHANAHAHYSRKWTBYERKTYVNNNGTMMXRMWAMVXKMDMDWBG 423
 QY 921 AATGGAATTTACACATCTGTGTTGTTACATATCCAGAAATGACGTAAGCTTTCATCTACC 980
 Db 424 TYNNNNNGRTYYGTTKKKKMMTYTYYKAAANCKMFAHDKCTHNNNTTMMKKTKYMNICY 483
 QY 981 AGAAGCTGAGCTGTAAAGTAGTAGTCTCCAAAAATGACAGTCCCTCTGTATCCAT 1040
 Db 484 WKSMTNGSHBBAAVTYTMMWBRVYAHANNMNDYWKACITWYKIVGCSKMMNNYAM 543
 QY 1041 TCACCTAATGATCATGTGCTCTATGAGAAAGAACAGAGAGAGACTCTCATTTCCCTGT 11000
 Db 544 YTKSSMNTSRYRYRKTKNNMSWRBDTSMGANNYAABHGYGKMTRMWBSHTWBH 603
 QY 1101 ACGGCTATTTAGTTTCTGTAGTATCTGCAATGAGGTGGTGACACAT-----TG 1155
 Db 604 RAGAAHYMBMMYBAKCHCMKRYAKKYAGAGSNNNNNNNNNNNNNNNNATCARDDY 663
 QY 1156 ATGAAAAAAACCTGATGACATCACTATTGATGTCAACATTCAGAAAGTATAGTCATA 1215
 Db 664 AASRYMAANAKWYKYYKBAANNAAYTTHANNWGCNNATTDTRTWMKNNNNNNAGTWKN 723
 QY 1216 GTAGACAGAGATGAATAAAGTAACTGATCTGTTAGATGATCAGAAAGTTACCTGTAGAG 1275
 Db 724 NNNNAKNASAAKNYAAAAVKAAKKWRANKRANGHADAABTTDKRNGATYTKTT 783
 QY 1276 ATCTCAAGCGAGCTATGCTGTCTAGTGAAGTCCAAAGCGAGAGTTGCCAAAGCAG 1335
 Db 784 NNNNTYGVYNTVNTAARDGMANNNNNNNNNNNNNNNNNSDMWWTWMAAYGYTNNNNNNNN 843
 QY 1336 CCAAGGTGAAGCAGAAAGTAAATAGATCCGCTCACTGATGAATCTCTGAGTCCAAATTA 1395
 Db 844 NAYAYMTWIKWYTTDDRRBBAVTNNNNNNRAVYAAYADDAVYSDTCDAMKRDATKK 903
 QY 1396 ACATGTGATGTAATAGACAAAAGAGAGATTGAGAACAGAGAGCTCCAGACCTAGC 1455
 Db 904 NNATTYRGTAMRTNNNNNNNTMKRYBYHAMNNNNNNNGMCTAHYMWVCAATTTGTC 963
 QY 1456 CTGACGCGACTTAACCATAGTATGAATCAAACTTAAATGAAAAATYTGAAAGTTTCA 1515
 Db 964 WNNCTTTRKYYRKNCTWYMTWTTTFTTYYAATRMATNNATGSMTCNAITGMKNNNYWTGW 1023
 QY 1516 TCTATGTAAGTACTCAAAATTTGTTCTGTGATATTGTTA 1555
 Db 1024 KTRWTAIRMTATRMKAMKVAATGSMNTNSIYARMAIKTIRA 1063
 RESULT 11
 US-09-489-847-73
 / Sequence 73, Application US/09489847
 / Patent No. 6476195
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al
 / TITLE OF INVENTION: 98 Human Secreted Proteins
 / FILE REFERENCE: PZ031P1
 / CURRENT APPLICATION NUMBER: US/09/489,847
 / CURRENT FILING DATE: 2000-01-24
 / EARLIER APPLICATION NUMBER: PCT/US99/17130
 / EARLIER FILING DATE: 1999-07-29

```

EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 73
LENGTH: 680
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (15)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (16)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-73

Query Match      2.7%; Score 57.8; DB 4; Length 680;
Best Local Similarity 80.0%; Pred. No. 5.5e-06;
Matches 68; Conservative 0; Mismatches 17; Indels 0; Gaps 0,

OY      1 CGGTGGGCGCCGCTCTAGAACTAGTGGATCCCGCGGATGCGAGAAATTGGCAGAGAAA 60
DB      33 CGGTGGGCGCCGCTCTAGAACTAGTGGATCCCGCGGATGCGAGAAATTGGCAGAGATA 92

OY      61 GTTCGGCGGAAAGTAAAGGCTCAG 85
DB      93 TTTCGCTGACCTAGAAAAGCCAC 117

RESULT 12
US-08-533-669A-5
Sequence 5, Application US/08533669A
Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 62..2029
US-08-533-669A-5

Query Match
Best Local Similarity 76.9%; Score 57.4; DB 2; Length 2040;
Pred. No. 1.4e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CGGTGGCGCCCGTTCTTGAAGTACTGATCCCGGGATGCAGAAATTCGGCAGAGAA 60
DB 3 CGGTGGCGCCCGCTCTGAAGTACTGATCCCGGGCTGCAGAAATTCGGCAGAGAA 62

QY 61 GTGGCGCGGAAAGTAAGAGGCTCACTGGGGA 91
DB 63 GCCTGACGACCCGCGCGTGTCTGGGCGAGGA 93

RESULT 13
US-09-183-861-5
Sequence 5, Application US/09183861
Patent No. 6355165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 62..2029
US-09-022-765-5

SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 62...2029
US-09-183-861-5

Query Match
Best Local Similarity 76.9%; Score 57.4; DB 3; Length 2040;
Pred. No. 1.4e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CGGTGGCGCCCGTTCTTGAAGTACTGATCCCGGGATGCAGAAATTCGGCAGAGAA 60
DB 3 CGGTGGCGCCCGCTCTGAAGTACTGATCCCGGGCTGCAGAAATTCGGCAGAGAA 62

QY 61 GTGGCGCGGAAAGTAAGAGGCTCACTGGGGA 91
DB 63 GCCTGACGACCCGCGCGTGTCTGGGCGAGGA 93

RESULT 14
US-09-022-765-5
Sequence 5, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 62..2029
US-09-022-765-5

Query Match
Best Local Similarity 76.9%; Score 57.4; DB 3; Length 2040;
Pred. No. 1.4e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY      1  CGGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGATGCAGAAATTCGGACGAGAA 60
      Db      3  CGGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGCTGCAGAAATTCGGACGAGAA 62
QY      61  GTCCGGCGGAGTAAGAGCTCACTGGGGA 91
      Db      63  GCCTGACGAGCCCGGCGTGTGGGCGAGGA 93
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RESULT 15

```
US-09-551-974A-5
; Sequence 5, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITRE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420CS
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Leishmania braziliensis
US-09-551-974A-5
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Best Local Similarity 76.9%; Pred No. 1.4e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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      Db      63  GCCTGACGAGCCCGGCGTGTGGGCGAGGA 93
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Search completed: December 25, 2004, 17:43:38
Job time : 189 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: December 25, 2004, 15:09:44 ; Search time 1124 Seconds

(without alignments)
10675.669 Million cell updates/sec

Title: US-08-917-710-1

Perfect score: 2155
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1242.8	57.7	4724	US-10-167-127-9	Sequence 9, Appl 1
2	1242.8	57.7	4724	US-10-717-597-14	Sequence 1, Appl 1
3	1047.8	48.4	2064	US-10-061-727-1	Sequence 1, Appl 1
4	1046.2	48.5	1077	US-10-215-211-5	Sequence 5, Appl 1
5	1046.2	48.5	1713	US-10-215-211-3	Sequence 3, Appl 1
6	1043	48.4	2703	US-10-287-162-39	Sequence 39, Appl 1
7	1043	48.4	2703	US-10-840-138-9	Sequence 9, Appl 1
8	1043	48.4	2709	US-10-282-162-41	Sequence 41, Appl 1
9	1043	48.4	2709	US-10-282-162-43	Sequence 43, Appl 1
10	1043	48.4	2709	US-10-840-138-11	Sequence 11, Appl 1
11	1043	48.4	2709	US-10-840-138-13	Sequence 13, Appl 1
12	1043	48.4	2733	US-09-313-942-27	Sequence 27, Appl 1

13	1043	48.4	2733	9	US-09-935-868-27	Sequence 27, Appl 1
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15	1043	48.4	2733	15	US-10-282-162-27	Sequence 27, Appl 1
16	1043	48.4	2733	18	US-10-840-138-1	Sequence 1, Appl 1
17	1043	48.4	2748	15	US-10-282-162-51	Sequence 51, Appl 1
18	1043	48.4	2748	18	US-10-840-138-21	Sequence 21, Appl 1
19	1043	48.4	2754	15	US-10-282-162-53	Sequence 53, Appl 1
20	1043	48.4	2754	15	US-10-282-162-55	Sequence 55, Appl 1
21	1043	48.4	2754	18	US-10-840-138-23	Sequence 23, Appl 1
22	1043	48.4	2754	18	US-10-840-138-25	Sequence 25, Appl 1
23	988.8	45.9	2748	15	US-10-282-162-45	Sequence 45, Appl 1
24	988.8	45.9	2748	18	US-10-840-138-15	Sequence 15, Appl 1
25	988.8	45.9	2754	15	US-10-282-162-47	Sequence 47, Appl 1
26	988.8	45.9	2754	15	US-10-282-162-49	Sequence 49, Appl 1
27	988.8	45.9	2754	18	US-10-840-138-17	Sequence 17, Appl 1
28	988.8	45.9	2754	18	US-10-840-138-19	Sequence 19, Appl 1
29	987.8	45.8	2703	15	US-10-282-162-33	Sequence 33, Appl 1
30	987.8	45.8	2703	18	US-10-840-138-3	Sequence 3, Appl 1
31	987.8	45.8	2709	15	US-10-282-162-35	Sequence 35, Appl 1
32	987.8	45.8	2709	15	US-10-282-162-37	Sequence 37, Appl 1
33	987.8	45.8	2709	18	US-10-840-138-5	Sequence 5, Appl 1
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35	794.2	36.9	3355	15	US-10-205-219-24	Sequence 24, Appl 1
36	790.2	36.7	2058	15	US-10-061-727-3	Sequence 3, Appl 1
37	367.4	17.0	443	9	US-09-880-107-3616	Sequence 3616, Ap
38	285.4	13.2	287	9	US-09-864-761-32830	Sequence 32830, A
39	223.6	10.4	271	9	US-09-880-107-3252	Sequence 3252, Ap
40	218.4	10.1	478	9	US-09-864-761-16315	Sequence 16315, A
41	168	7.8	1286	13	US-10-027-633-123144	Sequence 123144,
42	168	7.8	1286	13	US-10-027-633-123145	Sequence 123144,
43	168	7.8	1286	15	US-10-027-633-123144	Sequence 123144,
44	168	7.8	1286	15	US-10-027-633-123145	Sequence 123145,
45	167.4	7.8	169	9	US-09-864-761-21077	Sequence 21077, A

ALIGNMENTS

RESULT 1
US-10-167-127-9
Sequence 9, Application US/10167127
Publication No. US20030100031A1
GENERAL INFORMATION:
APPLICANT: DUFF, GORDON W.
TITLE OF INVENTION: INTERACTIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
FILE REFERENCE: NSA-026.01 (20974-2601)
CURRENT APPLICATION NUMBER: US/10/167,127
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 60/297,305
PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 4724
TYPE: DNA
ORGANISM: Homo sapiens
US-10-167-127-9

Query Match 57.7%; Score 1242.8; DB 15; Length 4724;
Best Local Similarity 99.8%; Pred. No. 7.1e-258; Indels 1; Gaps 1;
Matches 1255; Conservative 2; Mismatches 2;

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Qy 216 ATGTCATGATCATCATCACTAGAACTAGAACTAGACAGAGCCCTTAGAGCCTCATCTC 275

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Db	180	TTGCCCCCTCCCTTTAATATCTCAAGAGTGCACCTTCTGTGTGTGTAGTCACTCTAC	239
Qy	336	TTTTATAGAAATCCTGCGAAGTGAATGCCGACAAAGCGTCGGATACATCGGGGACTAGACAC	395
Db	240	TTTTATAGAAATCCTGCGAAGTGAATGCCGACAAAGCGTCGGATACATCGGGGACTAGACAC	299
Qy	396	ATGAGCGCAATCCAAAGTGTGTAAGATAGCGACCTCGCATCAAGTCCCACTCTTTGAA	455
Db	300	ATGAGCGCAATCCAAAGTGTGTAAGATAGCGACCTCGCATCAAGTCCCACTCTTTGAA	359
Qy	456	CACCTTTTGAATTTCACTACAGCACAGCCCATTCAGCTGGCCTTACTGTGATCTGTGAT	515
Db	360	CACCTTTTGAATTTCACTACAGCACAGCCCATTCAGCTGGCCTTACTGTGATCTGTGAT	419
Qy	516	TGCACTACAGAGACCGGGACCTTAGAGAGCCAAATTAACTTCGGCCTCCCGAGAACCGC	575
Db	420	TGCACTACAGAGACCGGGACCTTAGAGAGCCAAATTAACTTCGGCCTCCCGAGAACCGC	479
Qy	576	ATTAGTAGAGAGAAAGATGTGCTGTGTGTCGGGCCACTCTCTCTCAATGACATGCGAAC	635
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US-10-215-211-5
; Sequence 5, Application US/10215211
; Publication NO. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1077)
; OTHER INFORMATION:
; US-10-215-211-5

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Db	1021	GTTGCGAAAGCAGCCAAAGGTGAAACCAAGAAAG	1051

RESULT 5
US-10-215-211-3
US-10-215-211-3

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1  Publication No. US20030049255A1
2  -----
3  GENERAL INFORMATION:
4  APPLICANT: Sims, John E.
5  APPLICANT: Saltz, Dirk E.
6  TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
7  FILE REFERENCE: 3321-A
8  CURRENT APPLICATION NUMBER: US/10/215,211
9  CURRENT FILING DATE: 2002-08-07
10 PRIOR APPLICATION NUMBER: US 60/310,789
11 PRIOR FILING DATE: 2001-08-07
12 NUMBER OF SEQ ID NOS: 6
13 SOFTWARE: PatentIn version 3.1
14 SEQ ID NO 3
15 LENGTH: 1713
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (1)..(1713)
21 OTHER INFORMATION:
22 US-10-215-211-3

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Best Local Similarity	99.7%	Pred. No.	1.3e-215				
Matches 1048		Conservative	0	Mismatches	3	Indels	0
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Db	1	ATGACACTTCGTGCTGTGCTGAGTCTCACTCTTTATGGAATCCTCAAGTATGCC	60
QY	363	TCAGAACGCTGCCATGACTGGGACCTAGACACCTAGGACAAATCCAGTGTGAAGAT	422
Db	61	TCAGAACGCTGCCATGACTGGGACCTAGACACCTAGGACAAATCCAGTGTGAAGAT	120
QY	423	GAGCCAGCTGCATCGAAGTCCCACTCTTTGAACCTTTCTTGAATTCACCTACAGCACA	482

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Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTCTGATGAGTCTCTCGAATGAGGT 840
Qy 1143 TGTGAGCACTTGTAGTGAAGAAACCTGATGACATCACTATTTGATGTCCATTAGCA 1202
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Qy 1203 AGTATTAAGTCATAGTAGAACAAGAGTGAACCTGAACTGCACTTTTGAAGATTAAGAA 1262
Db 901 AGTATTAAGTCATAGTAGAACAAGAGTGAACCTGAACTGCACTTTTGAAGATTAAGAA 960
Qy 1263 GTTACTCTGAGGATCTGAGGAGAGTATGTCTGATGATAGAGTCCAAAGGCA 1322
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US-10-840-138-11
; Sequence 11, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsin Chieh
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-11
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Best Local Similarity 99.5%; Pred. No. 8e-215;
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 1 ATGAGTCTTCTGTGTGTAGTAGTCTCTACTTTATGGAATCTGCAAGTATGCC 60
Qy 363 TCAGAACGCTGCGATGACTGGGGACTTAACACCATGAGGCAATCCAAAGTGTGAAGAT 422
Db 61 TCAGAACGCTGCGATGACTGGGGACTTAACACCATGAGGCAATCCAAAGTGTGAAGAT 120
Qy 422 GAGCCAGCTCGCATGAAGGCCCATCTTTGAACACTTTGAAATTCATACAGACACA 482
Db 121 GAGCCAGCTCGCATGAAGGCCCATCTTTGAACACTTTGAAATTCATACAGACACA 180
Qy 483 GCCCATTCAGTGGCTTACTCTGATCTGTGATTTGAGACTTAAGCAGGACCGGAGCTTGAG 542
Db 181 GCCCATTCAGTGGCTTACTCTGATCTGTGATTTGAGACTTAAGCAGGACCGGAGCTTGAG 240
Qy 543 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTGCTGG 602
Db 241 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTGCTGG 300
Qy 603 TTCCGGCCCACTCTCTCATGACACTGGCAACTATACCTGATGTTAAGAAACACTACA 662
Db 301 TTCCGGCCCACTCTCTCATGACACTGGCAACTATACCTGATGTTAAGAAACACTACA 360
Qy 663 TATTGAGCAAGTTCATTTCCCTTGAAGTGTTCAAAAGAGAGTGTTCATATCC 722

Db 361 TATTGAGCAAGTTCATTTCCCTTGAAGTGTTCAAAAGAGAGTGTTCATATCC 420
Qy 723 CCCATGAACCTCCAGTGCATTAACCTGATATAGAAATGTGGATTCAGAGATCACTGT 782
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Db 961 GTTACTCTGAGGATCTGAGGAGAGTATGTCTGATGATAGAGTCCAAAGGCA 1020
Qy 1323 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1353
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1051
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; Sequence 13, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsin Chieh
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 99.5%; Pred. No. 8e-215;
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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RESULT 13
US-09-935-868-27
Sequence 27, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935, 868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 2733
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)...(2730)
US-09-935-868-27

Query Match 48.4%; Score 1043; DB 9; Length 2733;
Best Local Similarity 99.5%; Pred. No. 8, 1e-215;
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 121 GAGCAGCTCGCATCAAGTGCCTCTTTGAACACTCTTTGAATCACTACAGACA 180
Qy 483 GCCCATTCAGT 542
Db 181 GCCCATTCAGT 240
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RESULT 14
US-10-287-035-27
Sequence 27, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287, 035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935, 868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787, 835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313, 942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313, 942

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